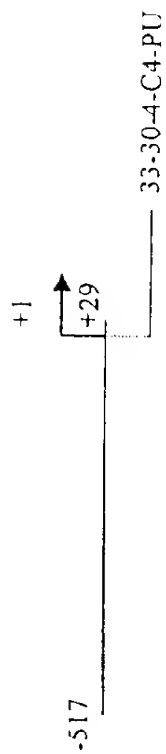
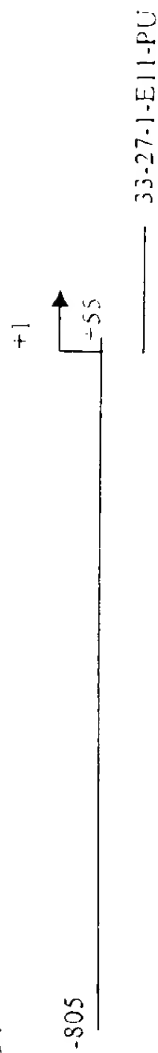


Promoter P13H2



Promoter P15B4



Promoter P29B6

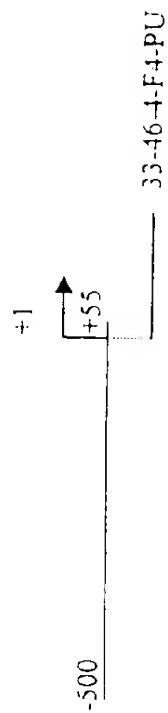


Figure 4

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME : GENSET SA
- (B) STREET : 24, RUE ROYALE
- (C) CITY: PARIS
- (E) COUNTRY : FRANCE
- (F) POSTAL CODE (ZIP) : 75008

(ii) TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS  
EXPRESSED IN PROSTATE

(iii) NUMBER OF SEQUENCES: 593

## (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy Disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: Win95
- (D) SOFTWARE: Word

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

## (ix) FEATURE:

- (A) NAME/KEY: Cap
- (B) LOCATION: 1
- (D) OTHER INFORMATION: m7Gppp added to 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCAUCCUAC UCCCAUCCAA UCCACCCUA ACUCCUCCCA UCUCCAC

47

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCAUCCUACU CCAUCCAAU UCCACCCUAA CUCCUCCCAU CUCCAC

46

## (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCAAGAATT CGCAGGAGAC CATTA

25

## (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TAATGGTCTC GTGCGAATTC TTGAT

25

## (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCGACAAGAC CAACGTCAAG GCCGC

25

## (2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCACCAGCAG GCAGTGGCTT AGGAG

25

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGTGATTCCT GGTACTTTGG ATGGC

25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTTGGTCTT GTTCTGGAGT TTAGA

25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCCAGGATGG GAGACAAGCC AATTT

25

(2) INFORMATION FOR SEQ ID NO: 10:



- (1) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGGGAGGAGG AAACAGCGTG AGTCC

25

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGGGAAAGG AAAAGACTCA TATCA

25

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGCAGCAACA ATCAGGACAG CACAG

25

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATCAAGAATT CCCACGAGAC CATTA

25

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATCGTTGAGA CTCGTACCAG CAGAGTCACG AGAGAGACTA CACGGTACTG GTTTTTTTTTT 60

TTTTTVN 67

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CCAGCAGAGT CACGAGAGAG ACTACACGG

29

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CACGAGAGAG ACTACACGGT ACTGG

25

(2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(261..376)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 166..281  
id N70479  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(380..486)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 54..160  
id N70479  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(110..145)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 403..438  
id N70479  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(196..229)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 315..348  
id N70479  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 90..140
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2  
seq LLLITAILAVAVG/FP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAATATRAC AGCTACAATA TTCCAGGGCC ATCCTACTTG CATTTCCTCAT AACAGCGTCA 60  
GAGAGAAAGA ACTGACTGAR ACGTTTGAG ATG AAG AAA GTT CTC CTC CTC ATC 113

```

Met Lys Lys Val Leu Leu Leu Ile
-15 -10

ACA GCC ATC TTG GCA GTG GCT GTW GGT TTC CCA GTC TTT CAA GAC CAG 161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
-5 1 5

GAA CGA GAA AAA AGA AGT ATC AGT GAC AGC GAT GAA TTA GCT TCA GGR 209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
10 15 20

WTT TTT GTG TTC CCT TAC CCA TAT CCA TTT CGC CCA CTT CCA CCA ATT 257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
25 30 35

CCA FTT CCA AGA TTT CCA TGG TTT AGA CST AAN TTT CCT ATT CCA ATA 305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
40 45 50 55

CCT GAA TCT GCC CCT ACA ACT CCC CTT CCT AGC GAA AAG TAAACAARAA 354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
60 65

GGAAAAGTCA CRATAAACCT GGTACCCIGA AATTGAAATT GAGUCASTTC CTTGAARAAT 414

CAAAATTCCT GTTAATAAAA RAAAAACAAA TGTAATTGAA ATAGCACACA GCATTCTCTA 474

GTCAATATCT TTAGTGATCT TCTTTAATAA ACATGAAAGC AAAAAAAAAA AA 526

```

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..17
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2  
seq LLLITAILAVAVG/FP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
1 5 10 15
Gly

```

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 260..464
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 153..357  
id H57434  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 98..164  
id H57434  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 35..92  
id H57434  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 454..485
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 348..379  
id H57434  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..545
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..428  
id N27248  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 65..369  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 41..345  
id H94779  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 61..399  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 6..344  
id H09880  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 408..458  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 355..405  
id H09880  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 60..399  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 56..395  
id H29351  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 393..432  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 391..430  
id H29351  
est

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 346..408  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.5  
seq SFLPSALVIWTSA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACTCCTTTTA GCATAGGGGC TTCGGCGCCA GCGGCCAGCG CTAGTCGGTC TGSTAAGTCC	60
CTGATGCCGA GTTCGGTCTC TCGCGTCTTT TCCTGGTCCC AGGCAAAGCG GASGNAGATC	120
GTCAAACGGC CTAGTGCTTC GCGCTTCCGG AGAAAATCAG CGGTCTAATT AATTCCTCTC	180
GTTTGTTGAA SCASITACCA AGAATCTTCA ACCCTTTCCC ACAAAAGCTA ATTGAGTAA	240

```

CGTTCCTGTT GASTACACGT TCCTGTTGAT TTACAAAAGG TGCAGGTATG AGCAGGTCG 300
AAGACTAACA TTTTGTGAAG TTGTAAACA GAAAACCTGT TAGAA ATG TGG TGG TTT 357
                                         Met Trp Trp Phe
                                         -20

CAG CAA GGC CTC AGT TTC CTT CCT TCA GCC CTT GTA ATT TGG ACA TCT 405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                      -10                      -5

GCT GGT TTC ATA TTT TCA TAC ATT ACT GCA GTA ACA CTC CAC CAT ATA 453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1                      5                      10                      15

GAC CCG CCT TTA CCT TAT ATC AGT GAC ACT GGT ACA GTA GGT CCA RAA 501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
      20                      25                      30

AAA TGC TTA TTT GGG GCA ATG CTA AAT ATT GCG GCA GTT TTA TGT CAA 549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
      35                      40                      45

AAA TAGAAATCAG GAARATAATT CAACTTAAAG AAKTTCATTT CATGACCAA 602
Lys

CTCTTCARAA ACATGTCTTT ACAAGCATAT CTCTTGATT GCTTTCTACA CTGTTGAATT 662

GTCTGGCAAT ATTTCTGCAG TGGAAAATTT GATTARMTA GTTCTTGACT GATAAATATG 722

GTAAGGTGGG CTTTTCCCCC TGTGTAATTG GCTACTATGT CTTACTGAGC CAAGTTGTAW 782

TTTGAAATAA AATGATATGA GAGTGACACA AAAAAAAAAA 822

```

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..21
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq SFLPSALVIWTS/AF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
      1                      5                      10                      15

```

Ile Trp Thr Ser Ala  
20

## (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(103..398)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..296  
id AA442893  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 185..295
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq LSYASSALSPLT/AP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

ATCACCTTCT TCTCCATCCT TSTCTGGGCC AGTCCCCARC CCAGTCCCTC TCCTGACCTG      60
CCCAGCCCAA GTCAGCCTTC AGCAGCGGCT TTTCTGCACA CAGATATTCG AGGCCTACCT      120
GGCATTCCAG GACCTCCGMA ATGATGCTCC AGTCCCTTAC AAGCGCTTCC TGGATGAGCG      180
TGGC ATG GTG CTG ACC ACC CTC CCC TTG CCC TCT GCC AAC AGC CCT GTG      229
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
      -35              -30              -25

AAC ATG CCC ACC ACT GGC CCC AAC AGC CTG AGT TAT GCT AGC TCT GCC      277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
      -20              -15              -10

CTG TCC CCC TGT CTG ACC GCT CCA AAK TCC CCC CGG CTT GCT ATG ATG      325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
      -5              1              5              10

CCT GAC AAC TAAATATCCT TATCCAAATC AATAAARWRA RAATCCTCCC TCCAAARWGG      384
Pro Asp Asn

TTTCTAAAAA CAAAAA AAA A      405

```



## (2) INFORMATION FOR SEQ ID NO: 22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..37
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq LSYASSALSPCLT/AP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn  
1 5 10 15  
Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu  
20 25 30  
Ser Pro Cys Leu Thr  
35

## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 149..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..183  
id AA397994  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 328..485  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 179..336  
                           id AA397994  
                           est

## (1x) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(182..496)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 14..328  
                           id AA399680  
                           est

## (1x) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 196..240  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.5  
                           seq ILSTVTALTFXA/LD

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

AAAAAATTGG TCCAGTTTT CACCCTGCCG CAGGGCTGGC TGGGGAGGGC AGCGCTTTAG      60
ATTAGCCGTG GCCTAGGCCG TTTAACGGGG TGACACGAGC NTGCAGGGCC GAGTCCAAGG      120
CCCGGAGATA GGACCAACCG TCAGGAATGC GAGGAATGTT TTTCTTCGGA CTCTATCGAG      180
GCACACAGAC AGACC ATG GGG ATT CTG TCT ACA GTG ACA GCC TTA ACA TTT      231
          Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
          -15                      -10                      -5

GCC ARA GCC CTG GAC GGC TGC AGA AAT GGC ATT GCC CAC CCT GCA AGT      279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
          1                      5                      10

GAG AAG CAC AGA CTC GAG AAA TGT AGG GAA CTC GAG ASC ASC CAC TCG      327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
          15                      20                      25

GCC CCA GGA TCA ACC CAS CAC CGA AGA AAA ACA ACC AGA AGA AAT TAT      375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
          30                      35                      40                      45

TCT TCA GCC TGAAATGAAC CCGGGATCAA ATGGTTGCTG ATCARAGCCC ATATTTAAAT      434
Ser Ser Ala

TGGAAAAGTC AAATTGASCA TTATTAAATA AAGCTTGTTC AATATGTCTC AAACAAATAA      494
AA                                                                 496

```

## (2) INFORMATION FOR SEQ ID NO: 24:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..15
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq ILSTVTALTFAXA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
  1           5           10           15
```

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 49..96
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.1  
seq LVLTLCCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```
AAAGATCCCT GCAGCCCGGC AGGAGAGAAG GCTGAGCCTT CTGGCGTC ATG GAG AGG      57
                                     Met Glu Arg
                                     -15

CTC GTC CTA ACC CTG TGC ACC CTC CCG CTG GCT GTG GCG TCT CCT GGC      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
      -10              -5              1

TGC GCC ACG ACG CCA GCT CGC AAC CTG AGC TGC TAC CAG TGC TTC AAG      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
      5              10              15

GTC AGC ACC TGG ACG GAG TGC CCG CCC ACC TGG TGC ACC CCG CTC GAC      201
```

```

Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20          25          30          35
CAA GTC TGC ATC TCC AAC GAG GTG GTC GTC TCT TTT AAA TGG AGT GTA      249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
          40          45          50
CGC GTC CTG CTC AGC AAA GGC TGT GCT CCC AGA TGT CCC AAC GAC AAC      297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
          55          60          65
ATG AAK TTC GAA TGG TCG CCG GGC CCC ATG CTG CAA GGC GTG ATC ACC      345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
          70          75          80
AGG CGC TGC TGT TCC TGG GCT CTC TGC AAC AGG GCA CTG ACC CCA CAG      393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
          85          90          95
GAG GGC CGC TGG GCC CTG CRA GGC GGG CTC CTG CTC CAG GAC CCT TCG      441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
100          105          110          115
AGG GGC ARA AAA ACC TGG GTG CCG CCA CAG CTG GGG CTC CCA CTC TGC      489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
          120          125          130
CTT CCC AWT TCC AAC CCC CTC TGC CCA RGG GAA ACC CAG GAA GGA      534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
          135          140          145
TAACACTGTG GGTCGCCCA CCGTGTGATT GGGACCACRA CTTCCACCTC TTGGARACAA      594
TAAACTCTCA TGCCCCCAAA AAAAAAAAAA      623

```

## (2) INFORMATION FOR SEQ ID NO: 26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..16
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.1  
seq LVLTLCTLPLAVA/SA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
1          5          10          15

```

## (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 32..73
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LWLLFFLVTAIHA/EL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

AACTTTGCCT TGTGTTTTCC ACCCTGAAAG A ATG TTG TGG CTG CTC TTT TTT CTG      55
                               Met Leu Trp Leu Leu Phe Phe Leu
                               -10

GTG ACT GCC ATT CAT GCT GAA CTC TGT CAA CCA GGT GCA GAA AAT GCT      103
Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala
-5                               1                               5                               10

TTT AAA GTG AGA CTT AGT ATC AGA ACA GCT CTG GGA GAT AAA GCA TAT      151
Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr
15                               20                               25

GCC TGG GAT ACC AAT GAA GAA TAC CTC TTC AAA GCG ATG GTA GCT TTC      199
Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe
30                               35                               40

TCC ATG AGA AAA GTT CCC AAC AGA GAA GCA ACA GAA ATT TCC CAT GTC      247
Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val
45                               50                               55

CTA CTT TGC AAT GTA ACC CAG AGG GTA TCA TTC TGG TTT GTG GTT ACA      295
Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr
60                               65                               70

GAC CCT TCA AAA AAT CAC ACC CTT CCT GCT GTT GAG GTG CAA TCA GCC      343
Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala
75                               80                               85                               90

ATA AGA ATG AAC AAG AAC CGG ATC AAC AAT GCC TTC TTT CTA AAT GAC      391
Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp
95                               100                               105

CAA ACT CTG GAA TTT TTA AAA ATC CCT TCC ACA CTT GCA CCA CCC ATG      439

```

```

Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met
      110                      115                      120

GAC CCA TCT GTG CCC ATC TGG ATT ATT ATA TTT GGT GTG ATA TTT TGC      487
Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys
      125                      130                      135

ATC ATC ATA GTT GCA ATT GCA CCA CTG ATT TCA TCA GGG ATC TGG CAA      535
Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln
      140                      145                      150

CGT ADA ARA AAG AAC AAA GAA CCA TCT GAA GCG GAT GAC GCT GAA RAT      583
Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Xaa
      155                      160                      165

AAK TGT GAA AAC ATG ATC ACA ATT GAA AAT GGC ATC CCC TCT GAT CCC      631
Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro
      175                      180                      185

CTG GAC ATG AAG GGA GGG CAT ATT AAT GAT GCC TTC ATG ACA GAG GAT      679
Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp
      190                      195                      200

GAG AGG CTC ACC CCT CTC TGAAGGGCTG TTGTTTCTGCT TCCTCAARAA      727
Glu Arg Leu Thr Pro Leu
      205

ATTAAACATT TGTTCCTGIG TGACTGCTGA GCATCCTGAA ATACCAAGAG CAGATCATAT      787

WTTTIGITTC ACCATTCTTC TTTTGTAAATA AATTTTGAAT GTGCTTGAAA AAAAAAAAAA      847

C                                                                 848

```

## (2) INFORMATION FOR SEQ ID NO: 28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..14
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LWLLFFLVTAIHA/EL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala
  1                      5                      10

```

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGGAAGATGG AGATAGTATT GCCTG

25

## (2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 26 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTGCCATGTA CATGATAGAG AGATTC

26

## (2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 546 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: promoter  
    (B) LOCATION: 1..517

(ix) FEATURE:

- (A) NAME/KEY: transcription start site  
    (B) LOCATION: 518

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site  
    (B) LOCATION: 17..25  
    (C) IDENTIFICATION METHOD: matinspector prediction  
    (D) OTHER INFORMATION: name CMYB\_01  
                            score 0.983  
                            sequence TGTCAGTTG

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(18..27)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MYOD\_Q6  
score 0.961  
sequence CCCAACTGAC

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(75..85)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name S8\_01  
score 0.960  
sequence AATAGAATTAG

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 94..104
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name S8\_01  
score 0.966  
sequence AACTAAATTAG

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(129..139)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name DELTAEF1\_01  
score 0.960  
sequence GCACACCTCAG

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(155..165)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA\_C  
score 0.964  
sequence AGATAAATCCA

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 170..178
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB\_01  
score 0.958  
sequence CITCAGTTG

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 176..189
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA1\_02  
score 0.959  
sequence TTGTAGATAGACA

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 180..190
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA\_C



score 0.953  
sequence ACATAGGACAT

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: 284..299  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name TAL1ALPHA47\_01  
score 0.973  
sequence CATAACAGATGCTAAG

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: 284..299  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name TAL1BETA47\_01  
score 0.983  
sequence CATAACAGATGGTAAG

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: 284..299  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name TAL1BETA1F2\_01  
score 0.978  
sequence CATAACAGATGGTAAG

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: complement(287..296)  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name MYOD\_Q6  
score 0.954  
sequence ACCATCTGTT

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: complement(302..314)  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name GATA1\_04  
score 0.953  
sequence TCAAGATAAAGTA

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: 393..405  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name IK1\_01  
score 0.963  
sequence AGTGGGAATTCC

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: 393..404  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name IK2\_01  
score 0.985  
sequence AGTGGGAATTC

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site

(B) LOCATION: 396..405  
 (C) IDENTIFICATION METHOD: matinspector prediction  
 (D) OTHER INFORMATION: name CREL\_01  
 score 0.982  
 sequence TGGGAATTCC

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
 (B) LOCATION: 423..436  
 (C) IDENTIFICATION METHOD: matinspector prediction  
 (D) OTHER INFORMATION: name GATA1\_02  
 score 0.950  
 sequence TCAATGATATGGCA

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
 (B) LOCATION: complement(478..489)  
 (C) IDENTIFICATION METHOD: matinspector prediction  
 (D) OTHER INFORMATION: name SRY\_02  
 score 0.951  
 sequence TAAACAAAACA

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
 (B) LOCATION: 486..493  
 (C) IDENTIFICATION METHOD: matinspector prediction  
 (D) OTHER INFORMATION: name E2F\_02  
 score 0.957  
 sequence TTTAGCGC

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
 (B) LOCATION: complement(514..521)  
 (C) IDENTIFICATION METHOD: matinspector prediction  
 (D) OTHER INFORMATION: name MZF1\_01  
 score 0.975  
 sequence TGAGGGGA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

TGAGTGGAGT GTTACATGTC AGTTGGGTTA AGTTTGTTAA TGTCAATCAA ATCTTCTATG   60
TCTTGATTGG CCTGCTAATT CTATTATTTT TGGAACTAAA TTAGTTTGAT GGTCTATTA   120
GTTATTGACT GAGGTGTGCT AATCTCCCAT TATGTGGATT TATCTATTTT TTCAGTTGTA   180
GATAGGACAT TGATAGATAC ATAAGTACCA GGACAAAAGC AGGGAGATCT TTTTCCAAA   240
ATCAGGAGAA AAAAATGACA TCTGGAAAAC CTATAGGGAA AGGCATAACA GATGGTAAGG   300
ATACTTTATC TTGAGTAGGA GAGCCTTCCT GTGGCAACGT GGACAAAGGA AGAGGTCGTA   360
GAATTGAGGA GTCAGCTCAG TTAGAAGCAG GGAGTTGGGA ATTCCGTTCA TGTGATTAG   420
CATCAGTGAT ATGGCAAATG TGGGACTAAG GGTAGTGATC ACAGGCTTAA AATTGTGTGT   480
TTTGTTTTAG CGCTGCTGGG GCATCGCCTT GGGTCCCCTC AAAGATATTC CCATGAATCT   540
CTTCAT                                     546

```

## (1) INFORMATION FOR SEQ ID NO: 32:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GTACGAGGGA CTGTGACCAT TGC

23

## (2) INFORMATION FOR SEQ ID NO: 33:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGTGACCAT TGCTCCCAAG AGAG

24

## (2) INFORMATION FOR SEQ ID NO: 34:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 861 base pairs
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: DOUBLE
  - (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: Genomic DNA

(1x) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 1..806

(1x) FEATURE:

- (A) NAME/KEY: transcription start site
- (B) LOCATION: 807

(1x) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(60..70)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name NFY\_Q6  
score 0.356  
sequence GGACCAATCAT

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 70..77
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MZF1\_01  
score 0.962  
sequence CCTGGGGA

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 124..132
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB\_01  
score 0.994  
sequence TGACCGTTG

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(126..134)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name VMYB\_02  
score 0.985  
sequence TCCAACGGT

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 135..143
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name STAT\_01  
score 0.968  
sequence TTCCTGGAA

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(135..143)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name STAT\_01  
score 0.951  
sequence TCCACGGAA

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(252..259)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MZF1\_01  
score 0.956  
sequence TTGGGGGA

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 357..369
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name IK2\_01  
score 0.965  
sequence GAATGGGATTC

## (ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 384..391
- (C) IDENTIFICATION METHOD: matinspector prediction

(D) OTHER INFORMATION: name MZF1\_01  
score 0.986  
sequence AGAGGGGA

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: complement(410..421)  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name SRY\_02  
score 0.955  
sequence GAAACAAAACA

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: 592..599  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name MZF1\_01  
score 0.960  
sequence GAAGGGGA

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: 618..627  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name MYOD\_Q6  
score 0.981  
sequence AGCATCTGCC

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: 632..642  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name DELTAEF1\_01  
score 0.958  
sequence TCCCACCTCC

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: complement(813..823)  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name S3\_01  
score 0.992  
sequence GAGGCAATTAT

## (ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: complement(824..831)  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name MZF1\_01  
score 0.986  
sequence AGAGGGGA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TACTATAGGG CACGCSTGGT CGACGGCCGG GCTGTTCTGG AGCAGAGGSC ATGTCAGTAA 60  
TCATTGGTCC CTGGGSAAGG TCTGGCTGGC TCCAGCACAG TGAGGCATTT AGGTATCTCT 120  
CGGTGACCGT TGGATTCCTG GAAGCAGTAG CTGTTCTGTT TGGATCTGCT AGGGACAGGS 180

```

CTCAGAGGGG TAGACAGGAG GGAAGGTCAG AGGAGAAGGS AGGSARGGCC CAGTCAGARG 240
GGAGCATGCC TTCCCCAAC CCTGGCTTSC YCTTGGYMAM AGGGGCKTTY TGGGMACTTR 300
AAYTCAGGGG CCAASCAGAA SCACAGGCC AKTCNTGGCT SMAAGCAGAA TAGCCTGAAT 360
GGGATTTGAG GTTAGNCAGG GTGAGAGGGG AGGCTCTCTG GCTTAGTTTT GTTTTGTTTT 420
CCAAATCAAG GTAAGTTGCT CCGTTCTGCT ACGGGCCTTG GTCTTGGGTT GTCCTCAGCC 480
AGTCGGAACT CCTAGCACT TTCAGGAGAG TGGTTTTAGG CCGTGGGGGC TGTTCGTTC 540
CAAGCAGTGT GAGAACATGG CTGGTAGAGG CTCTAGCTGT GTGCGGGGCC TGAAGGGGAG 600
TGGGTTCTCG CCGAAGAGC ATCTGCCCAT TTCCACCTT CCCTTCTCCC ACCAGAAAGCT 660
TGCCTGAGCT GTTGGACAA AAATCCAAAC CCCACTTGGC TACTCTGGCC TGGCTTCAGC 720
TTGGAACCCA ATACCTAGGC TTACAGGCCA TCCTGAGCCA GGGGCCTCTG GAAATCTCT 780
TCCTGATGGT CTTTAGGTT TGGGCACAAA ATATAATTGC CTCTCCCTC TCCATTTTC 840
TCTCTGGGA SCAATGGTCA C 861

```

## (2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

CTGGGATGGA AGGCACGGTA 20

```

## (2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

GAGACCACAC AGCTAGACAA 20

```

## (2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 555 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:  
    (A) NAME/KEY: promoter  
    (B) LOCATION: 1..500
- (ix) FEATURE:  
    (A) NAME/KEY: transcription start site  
    (B) LOCATION: 501
- (ix) FEATURE:  
    (A) NAME/KEY: TF binding-site  
    (B) LOCATION: 191..206  
    (C) IDENTIFICATION METHOD: matinspector prediction  
    (D) OTHER INFORMATION: name ARNT\_01  
                            score 0.964  
                            sequence GGACTCACGTGCTGCT
- (ix) FEATURE:  
    (A) NAME/KEY: TF binding-site  
    (B) LOCATION: 193..204  
    (C) IDENTIFICATION METHOD: matinspector prediction  
    (D) OTHER INFORMATION: name NMYC\_01  
                            score 0.965  
                            sequence ACTCACGTGCTG
- (ix) FEATURE:  
    (A) NAME/KEY: TF binding-site  
    (B) LOCATION: 193..204  
    (C) IDENTIFICATION METHOD: matinspector prediction  
    (D) OTHER INFORMATION: name USF\_01  
                            score 0.985  
                            sequence ACTCACGTGCTG
- (ix) FEATURE:  
    (A) NAME/KEY: TF binding-site  
    (B) LOCATION: complement(193..204)  
    (C) IDENTIFICATION METHOD: matinspector prediction  
    (D) OTHER INFORMATION: name USF\_01  
                            score 0.985  
                            sequence CAGCACGTGAGT
- (ix) FEATURE:  
    (A) NAME/KEY: TF binding-site  
    (B) LOCATION: complement(193..204)  
    (C) IDENTIFICATION METHOD: matinspector prediction  
    (D) OTHER INFORMATION: name NMYC\_01  
                            score 0.956  
                            sequence CAGCACGTGAGT
- (ix) FEATURE:  
    (A) NAME/KEY: TF binding-site  
    (B) LOCATION: complement(193..204)  
    (C) IDENTIFICATION METHOD: matinspector prediction

(D) OTHER INFORMATION: name MYCMAX\_02  
score 0.972  
sequence CAGCACGTGAGT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: 195..202  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name USF\_C  
score 0.997  
sequence TCACGTGC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: complement(195..202)  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name USF\_C  
score 0.991  
sequence GCACGTGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: complement(210..217)  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name MZF1\_01  
score 0.968  
sequence CATGGGGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: 397..410  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name ELK1\_02  
score 0.963  
sequence CTCTCCGGAAGCCT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: 400..409  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name CETS1P54\_01  
score 0.974  
sequence TCCGGAAGCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: complement(460..470)  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name AP1\_Q4  
score 0.963  
sequence AGTGACTGAAC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site  
(B) LOCATION: complement(460..470)  
(C) IDENTIFICATION METHOD: matinspector prediction  
(D) OTHER INFORMATION: name AP1FJ\_Q2  
score 0.961  
sequence AGTGACTGAAC

(ix) FEATURE:



(A) NAME/KEY: TF binding-site  
 (B) LOCATION: 547..555  
 (C) IDENTIFICATION METHOD: matinspector prediction  
 (D) OTHER INFORMATION: name PADS\_C  
 score 1.000  
 sequence TGTGGTCTC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

CTATAGGGCA CGCKTGGTCG ACGCCCCGGG CTGGTCTGGT CTGKTGTGGA GTCGGGTTGA   60
AGGACAGCAT TTGTACATC TGGTCTACTG CACCTTCCCT CTGCCGTGCA CTTGGCCTTT   120
KAWAAGCTCA GCACCGGTGC CCATCACAGG GCGGCAGCA CACACATCCC ATTACTCAGA   180
AGGAACTGAC GGACTCACGT GCTGCTCCGT CCCCATGAGC TCAGTGGACC TGTCTATGTA   240
GAGCAGTCAG ACAGTGCCTG CCATAGAGTG AGAGTTCAGC CAGTAAATCC AAGTGATTGT   300
CATTCCTGTC TGCATTAGTA ACTCCCAACC TAGATGTGAA AACTTAGTTC TTTCTCATAG   360
GTTGCTCTGC CCATGGTCCC ACTGCAGACC CAGGCACTCT CCGGAAGCCT GGAAATCACC   420
CGTGTCTTCT GCCTGCTCCC GCTCACATCC CACACTTGTG TTCAGTCACT GAGTTACAGA   480
TTTTGCCTCC TCAATTCTC TTGTCTTAGT CCCATCCTCT GTTCCCCTCG CCAGTTTGTG   540
TAGCTGTGTG GTCTC                                     555
  
```

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 16..84  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 11.4  
 seq VLALLLFVHYSNG/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

ACTTCCTGGT GCTGC ATG GTG TTC GTG CAC CTG TAC CTG GGT AAC GTG CTG   51
      Met Val Phe Val His Leu Tyr Leu Gly Asn Val Leu
      -20                               -15
GGG CTC CTG CTC TTC GTG CAC TAC AGC AAC GGC GAC GAA AGC AGC GAT   99
  
```

Ala Leu Leu Leu Phe Val His Tyr Ser Asn Gly Asp Glu Ser Ser Asp  
 -10 -5 1 5

CCC GGG CCC CAC CAC CGT GCC 120  
 Pro Gly Pro Gln His Arg Ala  
 10

## (2) INFORMATION FOR SEQ ID NO: 39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 202..288
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.3  
seq FLLCIFLICALA/AQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AAAAGTGGAA AATGGGAGGC ATGAAATACA TCTTTTCGTT GTTGTTCCTT CTTTGTCTAG 60  
 AAGGAGGCAA AACAGAGCAA GTAAACATT CAGAGACATA TTGCATGTTT CAAGACAAGA 120  
 AGTACAGAGT GGGTGAGAGA TGGCATCCTT ACCTGGAACC TTATGGGTTG GTTTACTGCG 180  
 TGAAGTGCAT CTGCTCAGAG A ATG GGA ATG TGC TTT GCA GCC GAG TCA GAT 231  
 Met Gly Met Cys Phe Ala Ala Glu Ser Asp  
 -25 -20  
 GTC CAA ATG TTC ATT GCC TTT CTC CTG TGC ATA TTC CTC ATC TGT GCT 279  
 Val Gln Met Phe Ile Ala Phe Leu Leu Cys Ile Phe Leu Ile Cys Ala  
 -15 -10 -5  
 GCC CTC GCT GCC CAG AAG AGT GGG 303  
 Ala Leu Ala Ala Gln Lys Ser Gly  
 1 5

## (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 203..280  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 11  
seq VLFLFLFWGVSLA/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

AAGGATGCTA TGCAAGTCAC TAATAAAGGA AGACACGGAC AGATGAACTT AAAAGAGAAG   60
CTTTAGCTGC CAAAGATTGG GAAAGGGAAA GGMCAAAAAA GACCCCTGGG CTACACGGCG   120
TAGGTGCAGG GTTCTCTACT GCTGTTCTTT TATGCTGGGA GCTGTGGCTG TAACCAACTA   180
GGAAATAACG TATGCAGCAG CT ATG GCT GTC AGA GAG TTG TGC TTC TCA AGA   232
                Met Ala Val Arg Glu Leu Cys Phe Ser Arg
                -25                               -20

CAA AGG CAA GTC CTG TTT CTT TTT CTT TTT TGG GGA GTG TCC TTG GCA   280
Gln Arg Gln Val Leu Phe Leu Phe Leu Phe Trp Gly Val Ser Leu Ala
-15                               -10                               -5

GGT TCT GGG TTT GGA CGT TAT TCG GTG ACC GGG   313
Gly Ser Gly Phe Gly Arg Tyr Ser Val Thr Gly
1                               5                               10

```

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 117..170  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.7  
seq LILLALATGLVGG/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

AAAGCCAGC CTACCTGCTG TAGCTGCCGC CAAATGATTC TCCGCGCCA CTGGWCCCC   60

```

```

AGAGCENMAG CCCAGAGCC TAGGAACCTG GGGTCCGCTG CTCCTCCCTC CAGGCC ATG   119
                                         Met

AGG ATT CTG CAG TTA ATC CTG CTT GCT CTG GCA ACA GGG CTT GTA GGG   167
Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly
      -15                      -10                      -5

GGA GAG ACC AGG ATC ATC AAG GGG TTC GAG TGC AAG CCT CAC TCC CAG   215
Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln
      1                      5                      10                      15

CCC TGG CAG GCA GCC CTG TTC GAG AAG ACC CGG CTA CTC TGT GGG GCG   263
Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala
                      20                      25                      30

ACG CTC ATC GCC CCC AGA TGG CTC CTG ACA GCA GCC CAC TGC CTC AAG   311
Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys
      35                      40                      45

CCC CGC TAC GGG   323
Pro Arg Tyr Gly
      50

```

## (2) INFORMATION FOR SEQ ID NO: 42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 94..147
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LILLALATGLVGG/ET

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

AAGAGGTGA GGTGGCTGGG GGACGGGAGG TCATCGGGCA GAGGTCTCAC AGCAGCCAAG   50

AAGCTGGGG CCCGCTCCTC CCCCTCCAG GCC ATG AGG ATT CTG CAG TTA ATC   114
                                         Met Arg Ile Leu Gln Leu Ile
                                         -15

CTG CTT GCT CTG GCA ACA GGG CTT GTA GGG GCA GAG ACC AGG ATC ATC   162
Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly Glu Thr Arg Ile Ile
      -10                      -5                      1                      5

AAT GGG TTC GAG TGC AAG CCT CAC TAC GAG CCC TGG CAG GCA GCC CTG   210

```

Lys Gly Phe Glu Cys Lys Pro His Xaa Gln Pro Trp Gln Ala Ala Leu  
                   10                  15                  20

TTC GAG AAG ACG CGG CTA CTC TGT GGG GCG ACG CTC ATC GCC CCC AGA 258  
 Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg  
                   25                  30                  35

TGG CTC 264  
 Trp Leu

## (2) INFORMATION FOR SEQ ID NO: 43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 23..112
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6  
                                   seq SLLLAVLVFFLFA/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTCTAGAACC CGACCCACCA CC ATG AGG TCC TGC CTG TGG AGA TGC AGG CAC 52  
                   Met Arg Ser Cys Leu Trp Arg Cys Arg His  
                   -30                  -25

CTG AGC CAA GGC GTC CAG TGG TCC TTG CTT CTG GCT GTC CTG GTC TTC 100  
 Leu Ser Gln Gly Val Gln Trp Ser Leu Leu Leu Ala Val Leu Val Phe  
 -20                  -15                  -10                  -5

TTT CTC TTC GCC TTG CCC TCT DNH AVT TRR KGD SCT CAA ACA AAG CCT 148  
 Phe Leu Phe Ala Leu Pro Ser Xaa Xaa Xaa Xaa Xaa Gln Thr Lys Pro  
                   1                  5                  10

TCC AGG CAT CAA CGC ACA GAG AAC ATT AAA GAA AGG TCT CTA CWG TCC 196  
 Ser Arg His Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Xaa Ser  
                   15                  20                  25

CTG GCA AAG CCT AAG TCC CAG GCA CCC ACA AGG GCA AGG AGG ACA ACC 244  
 Leu Ala Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr  
                   30                  35                  40

ATC TAT GCA GAG CCA GTG CCA GAG AAC AAT GCC CTC AAC ACA CAA ACC 292  
 Met Tyr Ala Glu Pro Val Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr  
                   45                  50                  55                  60

CAG CCC AAG GCC CAC ACC ACC GGA GAG AGA AGG AAA GGA 331

Gln Pro Lys Ala His Thr Thr Gly Asp Arg Arg Lys Gly  
65 70

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 167..220
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6  
seq XILLALATGLVGG/EI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

AATGTGGGAC GTGGCTTTGT TCTAATAAGA CGAAGGGTGG AGTGCAGGCT TGGAAAGCAG   60
GAGAGCTCAG CCTACGTCTT TAATCCTCCT GCCCACCCTT TGGRTTCTGT CTCCACTGGG   120
RCTCAAGASV AGGACCCTGG GGGCCCGCTC CTCCCCCCTC CAGGCC ATG AGG ATT   175
                               Met Arg Ile
CTG CAG TKA ATC CTG CTT GCT CTG GCA ACA GGG CTT GTA GGG GGA GAG   223
Leu Gln Xaa Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly Glu
-15          -10          -5          1
ATC AGG ATC ATC AAG GGG TTC GAG TGC AAG CCT CAC TCC CAG CCC TGG   271
Ile Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro Trp
          5          10          15
CAG GCA GCC CTG TTC GAG AAG ACG CCG CTA CTA CTG TGG GGC GAC GCT   319
Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Leu Trp Gly Asp Ala
          20          25          30
CAT CGC CCC CAG ATG GCT CCT GAC AGC AGC CCA CTG CCT CAA GCC CCG   367
His Arg Pro Gln Met Ala Pro Asp Ser Ser Pro Leu Pro Gln Ala Pro
          35          40          45
CTA CAT AGT TCA CCT GGG GCA GCA CAA CCT CCA GAA GGA   406
Leu His Ser Ser Pro Gly Ala Ala Gln Pro Pro Glu Gly
          50          55          60

```

## (2) INFORMATION FOR SEQ ID NO: 45:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 35..148
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.4  
seq LWLLKLKLVSTXWA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

ATACGTGTTTA TAAGCAACCT TGGTTTACACA TAGT ATG TTG SAA GAG TGT GGG GCT    55
                               Met Leu Glu Glu Cys Gly Ala
                               -35

GGG GTT GAT TTA GGA TTT GGA GGT GTA AAG TTT GGC AGT GAG ACA CCA    103
Gly Val Asp Leu Gly Phe Gly Gly Val Lys Phe Ala Ser Glu Thr Pro
-30                      -25                      -20

AAC CTT CTC TGG CTG CTT TTA AAA CTK GTA AGT ACC YCT TGG GCT GTA    151
Asn Leu Leu Trp Leu Leu Lys Leu Val Ser Thr Xaa Trp Ala Val
-15                      -10                      -5                      1

AGA GTG ACT TTG ATC ATA TTT AAC AAC CAG GCA AGG                    187
Arg Val Thr Leu Ile Ile Phe Asn Asn Gln Ala Arg
                    5                      10

```

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 249..317
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.2  
seq RCLLLALVAESSS/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

ATCTACTATA AAATCGATAG AAAAAAAGT TCTTTATGGC TACTGGTGAAG CTTTATATCC   60
TGATACGCGCT GAAGTGGCA GCCCACAGTC AGTGTGCTTG ATGACTCTTA SATTGAAAGA   120
CCGCTCTTCC AAAGACACGT GCCTGTGCTC TGCAAGTTK ATGTGCCATC TTGGAAGGCT   180
CAAAGCAGTT TCTTCTGTT GCTGAAGATA CCAGTGACCA CAGAAGGGCT TTTACCCCT   240
TCTCCGTA ATG ATC GCT TGC AGC ATT AGA GAG TTG CAC AGA TGT CTK TTG   290
      Met Ile Ala Cys Ser Ile Arg Glu Leu His Arg Cys Leu Leu
              -20              -15              -10

TTA GCT TTG GTG GCG GAG TCA TCC TCA CAG ACC CAG GGG   329
Leu Ala Leu Val Ala Glu Ser Ser Ser Gln Thr His Gly
              -5              1

```

## (2) INFORMATION FOR SEQ ID NO: 47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 182..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.2  
seq SLVLCLLSATVFS/LQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

AGTTTTTTCC AGCTCCTGGG CGAATCCAC ATCTGTTTCA ACTCTCCGCC GAGGGCGAGC   60
AGGAGCGAGA GTGTGTCGAA TCTSCGAGTG AAGAGGGAAC SAGGGGAAAA GAAACAAAGC   120
CACAGACGCA ACTTGAGACT CCCGCATCCC AAPAGAAGCA CCAGATCAGC AAAAAAAGAA   180
S ATG GGC CCC CCG AGC CTC GTG CTG TGC TTG CTG TCC GCA ACT GTG TTC   229
      Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe
              -15              -10              -5

TCC CTG CAG GGT GGA AGC TCG GCG TTC CTG TCG CAC CAC CGC CCC GGG   277
Ser Leu Gln Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Pro Gly
      1              5              10              15

```

## (2) INFORMATION FOR SEQ ID NO: 48:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 17..121
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9  
seq AMWLLLLWGVQLQX/XP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

AGATGTCCAG TTCCAG ATG CCT GGA CCC AGA GTG TGG GGG AAA TAT CTC TGG      52
      Met Pro Gly Pro Arg Val Trp Gly Lys Tyr Leu Trp
      -35                      -30                      -25

AGA AGC CCT CAC TCC AAA GGC TGT CCA GGC CCA ATG TGG TGG CTG CTT      100
Arg Ser Pro His Ser Lys Gly Cys Pro Gly Ala Met Trp Trp Leu Leu
      -20                      -15                      -10

CTC TGG GGA GTC CTC CAG GST TKG CCC AAC CCG GGG CTC CGT CCT CTT      148
Leu Trp Gly Val Leu Gln Xaa Xaa Pro Asn Pro Gly Leu Arg Pro Leu
      -5                      1                      5

GGC CAA AGA GCT ACC CCA GCA GCT GAC ATC CCC CCG GTA CCC AGA GCC      196
Gly Xaa Arg Ala Thr Pro Ala Ala Asp Ile Pro Arg Val Pro Arg Ala
      10                      15                      20                      25

GTA TGG CAA AGG CCA AGA GAG CAA CAC GGA CAT CAA GGC TCC AGA GGG      244
Val Trp Gln Arg Pro Arg Glu Gln His Gly His Gln Gly Ser Arg Gly
      30                      35                      40

CTT TGC TGT GAG GCT CGT CTT CCA GGA CTT CGA CCT GGA GCC GTC CCA      292
Leu Cys Cys Glu Ala Arg Leu Pro Gly Leu Arg Pro Gly Ala Val Pro
      45                      50                      55

GGA CTG TGC AGG GGA CTC TGT CAC AAT CTC ATT CGT CCG TTC GGA TCC      340
Gly Leu Cys Arg Gly Leu Cys His Asn Leu Ile Arg Arg Phe Gly Ser
      60                      65                      70

AAG CCA CTC GGG
Lys Pro Leu Gly
      75

```

## (xii) INFORMATION FOR SEQ ID NO: 49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs

(B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 151..216  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.8  
 seq LLTLALLGGPTWX/XK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

AAGAGCCCCA CGGCCAGCTC CTCCTGTTC CCCTGGCGGG CCCTCGCTTC TTCCTTCTGG    60
ATGGGGGGCCC AGGGGGCCAG GAGAGTATAA ASGSWKDKG GARGGGTGCC CGGCACAACC    120
AGACGCCCAG TCACAGGCGA GAGCCCTGGG ATG CAC CGG CCA GAG GCC ATG CTG    174
                               Met His Arg Pro Glu Ala Met Leu
                               -20                               -15

CTG CTG CTC ACG CTT GCC CTC CTG GGG GGC CCC ACC TGG GMA SGG AAG    222
Leu Leu Leu Thr Leu Ala Leu Leu Gly Gly Pro Thr Trp Xaa Xaa Lys
                               -10                               -5                               1

ATG TAT GGC CCT GGA GGA GGC AAG TAT TTC AGC ACC ACT GAA GAC TAC    270
Met Tyr Gly Pro Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr
                               5                               10                               15

GAC CAT GAA ATC ACA GGG CTG CGG GTG TCT GTA GGT CKT CTC CTG GTG    318
Asp His Glu Ile Thr Gly Leu Arg Val Ser Val Gly Xaa Leu Leu Val
                               20                               25                               30

AAA AGT GTC CAG GTG AAA CTT GGA GAC TCC TGG GAC GTG AAA CTG GGA    366
Lys Ser Val Gln Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly
                               35                               40                               45                               50

GGC CTT AGG TGG GAA TAC CCA GGA AGT CAC CCT GCA GCC AGG CGA ATA    414
Gly Leu Arg Trp Glu Tyr Pro Gly Ser His Pro Ala Ala Arg Arg Ile
                               55                               60                               65

CAT CAC AAA AGT CTT TGT CGC TTC CAA GCT TTC CTC    450
His His Lys Ser Leu Cys Arg Phe Gln Ala Phe Leu
                               70                               75

```

(2) INFORMATION FOR SEQ ID NO: 50:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 5..49
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6  
seq SVSLALLSGWVGS/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```
AGAC ATG GTA AGT GTG AGT TTA GCG CTG CTG TCC GGA TGG GTT GGT AGC      49
Met Val Ser Val Ser Leu Ala Leu Leu Ser Gly Trp Val Gly Ser
-15                      -10                      -5

AGA CAG GGT GGA GTA GGG TTA AGC ACA CTG GTC ACC TTA GCA TTG CTT      97
Arg Gln Gly Gly Val Gly Leu Ser Thr Leu Val Thr Leu Gly Leu Val
1                      5                      10                      15

TCC TGG TGC TGG AGA ATG GTT AGG ACA CAG GCC TTG GAA GGT TTT TTG      145
Ser Trp Cys Trp Arg Met Val Arg Thr Gln Ala Leu Gln Gly Phe Leu
20                      25                      30

AGT GTG AAA TAT TAC TCA GCG TTT TCT GCA GAC CTG                        181
Ser Val Lys Tyr Tyr Ser Ala Phe Ser Ala Asp Leu
35                      40
```

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 129..275
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq IVFLLLRVSPCLG/PS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```
AAAGATATCAG TGTCTTGTTC TCACTTACAT CCTACTTACA AAGTGAGGCT TATTACAGA      60
```

ATAAAGCCTT CCTTTAAAGC TTTATAATAA TCATATTTAT TAATAATGCT GTTGTSCATA 120  
 CTTATAGT ATG CAT ATA TTC AGC ATA TGT TGC ATG TST TCA GAA TTA CAT 170  
     Met His Ile Phe Ser Ile Cys Cys Met Xaa Ser Glu Leu His  
                     -45                    -40

AAG ATG AAA TCC CTT TCA TTG CAA CTT GCA AGT GAG AAA AGA TCC TTA 218  
 Lys Met Lys Ser Leu Ser Leu Gln Leu Ala Ser Glu Lys Arg Ser Leu  
 -35                    -30                    -25                    -20

GTG GCT CTG GTG GAA GAA ATA GTA TTT CTT CTT CTC AGG GTG TCT CCC 266  
 Val Ala Leu Val Glu Glu Ile Val Phe Leu Leu Arg Val Ser Pro  
                     -15                    -10                    -5

TGC CTT GGC CCC TCC CAB AAG CCC CGG 293  
 Cys Leu Gly Pro Ser Xaa Lys Pro Arg  
                     1                    5

## (2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 258..308
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq VSALLMAWFGVLS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

AGCGCCGAGC TGACCGGGCG ACGCCGCGGG AGGTTCTGGA AACGCCGGGA GCTGCGAGTG 60  
 TCCAGACATC CTTGTGGAAC CAGGCGTTGT KTTTCCTTGG CAGCTGCGGA GACCCGTGAT 120  
 AATTCGTAA CTAATTCAAC AAACGGGACC CTTCTGTGTG CCAGAAACCG CAAGCAGTTG 180  
 CTAACCCAGT GGGACAGGCG GATTGGAAGA GCGGGAAGGT COTGGCCAG ACCASTGTGA 240  
 CACTTCCCTC TGTGACC ATG AAA CTC TGG GTG TCT GCA TTG CTG ATG GCC 290  
     Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala  
                     -15                    -10

TGG TTT GST GTC CTG AGC TGT GTG CAG ACC GGG 323  
 Trp Phe Gly Val Leu Ser Cys Val Gln Thr Gly  
     -5                    1                    5

## (2) INFORMATION FOR SEQ ID NO: 53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 92..157
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq LLLPLMLMSMVSS/SL

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

AGACCTGAGT CATCCCCAGG GATCAGGAGC CTCCAGCAGG GAACCTTCCA TTATATTCTT   60
CAAGCAACTT ACAGCTGCAC CGACAGTTGC G ATG AAA GTT CTA ATC TCT TCC   112
                               Met Lys Val Leu Ile Ser Ser
                               -20

CTC CTC CTG TTG CTG CCA CTA ATG CTG ATG TCC ATG GTC TCT AGC AGC   160
Leu Leu Leu Leu Leu Pro Leu Met Leu Met Ser Met Val Ser Ser Ser
-15                -10                -5                1

CTG AWT CSA GGG GTC GCC AGA GGC CAC AGG GAC CGA GGC CAG GCT TCT   208
Leu Xaa Pro Gly Val Ala Arg Gly His Arg Asp Arg Gly Gln Ala Ser
      5                10                15

AGG AGA TGG CTC CAG GAA GGC GGA CTG   235
Arg Arg Trp Leu Gln Glu Gly Gly Leu
      20                25

```

## (2) INFORMATION FOR SEQ ID NO: 54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: 159..224  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.3  
 seq LLLPLMLMSMVSS/SL

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

ACTGTTCTCG CCTCAAATG GGAACGCTGA CCTGGGACTA AASCATAGAC CACGAGGCTG    60
AGTATCCTGA CCTGASTCAT CCCCAGGGAT CAGGAGCCTC CAGCAGGGAA CATTGCATTA   120
TATTCTTCAA GCAACTTACA GCTGCACCGA CAGTTGGG ATG AAA GTT CTA ATC TCT   176
                               Met Lys Val Leu Ile Ser
                               -20

TCC CTC CTC CTG TTG CTG CCA CTA ATG CTG ATG TCC ATG GTC TCT AGC    224
Ser Leu Leu Leu Leu Leu Pro Leu Met Leu Met Ser Met Val Ser Ser
   -15                      -10                      -5

AGC CTG AAT CCA GGG GTC GCC AGA GGC CAC AGG GAC CGA GGC CAG GCT    272
Ser Leu Asn Pro Gly Val Ala Arg Gly His Arg Asp Arg Gly Gln Ala
   1                      5                      10                      15

TCT AGG AGA TGG CTC CAG GAA GGC GGC CAA GAA TGT SAG TGC AAA GAT    320
Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln Glu Cys Glu Cys Lys Asp
          20                      25                      30

TGG TTC CTG AGA GCC CCG AGA AGA AAA TTC ATG ACA GTG TCT GCG    365
Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe Met Thr Val Ser Gly
          35                      40                      45
  
```

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 99..140
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2  
seq LLLLQLSLPSPTS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

AAVVAATGATG TGCCTGGGAA CTGCAATCAT TTGAAAAGAT AGCAATCAAG CATTCTTTTC    60
AGAGCTCTGT TCAATTTTCA GCGCTTTTGG TTCTGCTG ATG GTT TTG CTC GTT CAA   116
  
```

Met Leu Leu Leu Leu Gln  
-10

TTA TCT CTS CCT TCT CCC ACC TCC TCT CCG 146  
Leu Ser Leu Pro Ser Pro Thr Ser Ser Pro  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 25..75
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1  
seq LSFKLLLLAVALG/FF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

AGCCCCTGCT GCTCTGGGCA GAGG ATG CTG AAG ATG CTC TCC TTT AAG CTG 51  
Met Leu Lys Met Leu Ser Phe Lys Leu  
-15 -10

CTG CTG CTG GCC GTG GCT CTG GGC TTC TTT GAA GGA GAT GCT AAG TTT 99  
Leu Leu Leu Ala Val Ala Leu Gly Phe Phe Glu Gly Asp Ala Lys Phe  
-5 1 5

GGG GAA 105  
Gly Glu  
10

## (2) INFORMATION FOR SEQ ID NO: 57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 138..203
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq LLTLALLGXXXWA/GK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

AGCTCCTTCC TGTTCCTCTG GCGGCCCTCT GCTTCTTCTT TCTGGATGGG GGCCAGGGG    60
GCCAGGAGA GTATAAAGGC GATGTGGAGG GTGCCGGCA CAACCAGACG CCCAGTCACA    120
GGGCGGAGAG CHSTGRG ATG CAC CGG CCA GAG GCC ATG CTG CTG CTG CTC    170
           Met His Arg Pro Glu Ala Met Leu Leu Leu Leu
           -20                               -15

ACG CTT GCC CTC CTG GGG GRC MCC AMC TGG GCA GGG AAG ATG TAT GGC    218
Thr Leu Ala Leu Leu Gly Xaa Xaa Xaa Trp Ala Gly Lys Met Tyr Gly
-10                               -5                               1                               5

CCT GGA GGA GGC AAG TAT TTC AGC ACC ACT GAA GAC TAC GAC CAT GAA    266
Pro Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu
           10                               15                               20

ATC ACA GGG CTG CGG GTG TCT GTA GGT CTT CTC CTG GTG AAA AGT GTC    314
Ile Thr Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val
           25                               30                               35

CAG GTG AAA CTT GGA GAC TCC TGG GAC GTG                                344
Gln Val Lys Leu Gly Asp Ser Trp Asp Val
           40                               45

```

## (2) INFORMATION FOR SEQ ID NO: 58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 58..105
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq VSAVLCVCAAAWC/SQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

AAGAGCAGGG CTGCATTTCG AACAGGAGCT GCGAGCACAG TGCTGGCTCA CACCAAG    57

```



```

ATG CTC AAG GTG TCA GCC GTA CTG TGT GTG TGT GCA GCC GCT TGG TGC      105
Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp Cys
   -15                      -10                      -5

AGT CAG TCT CTC GCA GGT GGC GCG GCG GTG GCT GCA GCC GGG GGG CGG      153
Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly Gly Arg
   1                      5                      10                      15

TCG GAC GGC GGT AAT TTT CTG GAT GAT AAA CAA TGG CTC ACC ACA ATC      201
Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Thr Ile
                20                      25                      30

TCT CAG TAT GAC AAG GAA GTC GGA CAG TGG AAC AAA TTC CCA GAC GAT      249
Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys Phe Arg Asp Asp
                35                      40                      45

GAT TAT TTC CGC ACT GGG                                              257
Asp Tyr Phe Arg Thr Gly
   50

```

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 124..174
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq VLWLISFFFTFDG/HG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

AAGCATAAGA AGTGATTGAG CCACAAGTAT ACTGAAGGAA GGGCTCCCTC GAGTTGTGGT      60
GTGAGAGAGAT AATCACCAG TCACAGACTA TGCACCCGAC TGCTGCTGTT CAGTCCAGGG      120

AAA ATG AAA GTT GGA GTG CTG TGG CTC ATT TCT TTC TTC ACC TTC ACT      168
Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr
   -15                      -10                      -5

GAC GGC CAC GGT GGC TTC CTG GGG AAA AAT GAT GGC ATC AAA ACA AAA      216
Asp Gly His Gly Gly Phe Leu Gly Lys Asn Asp Gly Ile Lys Thr Lys
   1                      5                      10

AAA GAA CTC ATT GTC AAT AAG AAA AAA CAT CTA GGC CTC GCG      258
Lys Glu Leu Ile Val Asn Lys Lys Lys His Leu Gly Leu Gly

```

15

20

25

## (2) INFORMATION FOR SEQ ID NO: 60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 155..202
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7  
seq ILLDLICLLFITA/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

ACTGAAATAG GAAAGTAAGA TTTATACCCA TTATTCAGCC AAAATCTGTT TTTCTTTAAC    60
TTCTACCCAT TGTTCCCTAAG TCTGCCCTCT GGGGGCTGTA GAAATAATG AAGATGATGT   120
TATTAATGAT AACCAGTGCT TGCTGTAACC AGTT ATG TGC ATT ATT TTA TTG GAT    175
                               Met Cys Ile Ile Leu Leu Asp
                               -15                               -10

TTA ATT TGT TTA CTC TTT ATA ACA GCA TGT GTG GGG                        211
Leu Ile Cys Leu Leu Phe Ile Thr Ala Cys Val Gly
          -5                               1

```

## (2) INFORMATION FOR SEQ ID NO: 61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 131..307
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6

seq FMVFGSFFPLISC/QP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```

ACATGGATTG ATTTGTTATT TGGGGATTAA ATTAGGCAGG GCACATAGTA GGGCCTCCTT    60
GGATGTTTGA TGGCTGTTGA ATGAACGTAA GTGAATCTGT TCAGTTTTAG GGTTTTATTC    120
CATTTTTGAT ATG GAT TGT GCC AGT ATA TCT GTA AAG TTC ACT TCT ATG    169
      Met Asp Cys Ala Ser Ile Ser Val Lys Phe Thr Ser Met
            -55                      -50

GCT ACC ATG CAT GAC TTG AST CAG TTC TGG GCT TCT AGA GGA GAG GTT    217
Ala Thr Met His Asp Leu Ser Gln Phe Trp Ala Ser Arg Gly Glu Val
      -45                      -40                      -35

ACA AAC TGG TGG CCA GTA GGA CAA ACT ASC CTA CCA CTG TTT TAT TTG    265
Thr Asn Trp Trp Pro Val Gly Gln Thr Ser Leu Pro Leu Phe Tyr Leu
      -30                      -25                      -20                      -15

GCT TTC ATG GTG TTT GST TCT TTT TTT CCT TTA ATT TCC TGC CAG CCC    313
Ala Phe Met Val Phe Gly Ser Phe Phe Pro Leu Ile Ser Cys Gln Pro
            -10                      -5                      1

GGG                                                                316
Gly

```

## (2) INFORMATION FOR SEQ ID NO: 62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 147..206
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq LVVLFGITAGATG/AK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

ACCTTTGCAC TAGCAGTAGC AAGGAAGGGG GGTGGGCGCT CTTTCTTTTT CTCTTAGAAG    60
AGGGTTTAGC ACAGGTTTTT TCGTTCTCAC TTCCACACCA CCTTACCGCC TCCCGACCCC    120
CGCTCTCCCC CTGCGCACCT ATCGTC ATG ACC GCC TCT CCG GAT TAC TTG GTG    173
      Met Thr Ala Ser Pro Asp Tyr Leu Val
            -20                      -15

```

```

GTG CTT TTT GGG ATC ACT GCT GGG GGC ACC GGG GGC AAG CTA GGC TCG      221
Val Leu Phe Gly Ile Thr Ala Gly Ala Thr Gly Ala Lys Leu Gly Ser
-10                      -5                      1                      5

GAT GAG AAG GAC TTG ATC CTG CTG TTT TGG AAA GTC GTG GAT CTN GCC      269
Asp Glu Lys Glu Leu Ile Leu Leu Phe Trp Lys Val Val Asp Leu Ala
10                      15                      20

AAC AAG AAG GTG GGA CAG TTG CAG GAA BKA HGN TTA GAC CCG ATC TGG      317
Asn Lys Lys Val Gly Gln Leu His Glu Xaa Xaa Leu Asp Arg Ile Trp
25                      30                      35

```

## (2) INFORMATION FOR SEQ ID NO: 63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 46..90
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq CVLVLAAAAGAVA/VF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

AAGCGGCTGG TCCCCGGAAG TTGGACGCAT GCGCCGTTTC TCTGC ATG GTG TGC GTT      57
Met Val Cys Val
-15

CTC GTT CTA GCT GCG GCC GCA GGA GCT GTG GCG GTT TTC CTA ATC CTG      105
Leu Val Leu Ala Ala Ala Ala Gly Ala Val Ala Val Phe Leu Ile Leu
-10                      -5                      1                      5

CGA ATA TGG GTA GTG CTT CGT TCC ATG GAC GTT ACG CCC CGG GAG TCT      153
Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr Pro Arg Glu Ser
10                      15                      20

CTC AGT ATC TTG GTA GTG GCT GGG TCC GGT GGG CAT ACC ACT GAG ATC      201
Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His Thr Thr Glu Ile
25                      30                      35

CTG AGG CTG CTT GGG AGC TTG TCC AAT GCC TAC TCA CCT AGA CAT TAT      249
Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser Pro Arg His Tyr
40                      45                      50

GTC ATT GCT GAC ACT GAT GAA ATG AGT GCC ACG      282
Val Ile Ala Asp Thr Asp Glu Met Ser Ala Thr

```

55

60

## (2) INFORMATION FOR SEQ ID NO: 64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 48..179
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5  
seq LMIPLLLTPITA/TS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

ACAACTCAAG CCAGACAGGC AGCAATTCCA GACTCGAAAG AGGCCTT ATG AAG AAA      56
                                         Met Lys Lys

ACC GGG GAC GGG GGT ACT TTG AGC ACC GAG AGG ATA GGA GGG GCC GCT      104
Thr Gly Asp Gly Gly Thr Leu Ser Thr Glu Arg Ile Gly Gly Ala Ala
-40                               -35                               -30

CTC CTC AGC CTC CTG CTG AAG AGG ATG AAG ATG ACT TTG ATG ATA CCC      152
Leu Leu Ser Leu Leu Leu Lys Arg Met Lys Met Thr Leu Met Ile Pro
-25                               -20                               -15                               -10

TTG TTG CTA TTG ACA CCT ATA ACT GCG ACC TCC ACT TCA AGG TGG CCC      200
Leu Leu Leu Leu Thr Pro Ile Thr Ala Thr Ser Thr Ser Arg Trp Pro
-5                               1                               5

GAG ATC GGA GTA GTG GCT ATC CGC TCA CAA TTG AGG GCT TTG CAT ACC      248
Glu Ile Gly Val Val Ala Ile Arg Ser Gln Leu Arg Ala Leu His Thr
10                               15                               20

TGT GGT CAG GAG CCC GTG CCA GCT ATG GGG TCA GAA GGG GCC GCG      293
Cys Gly Gln Glu Pro Val Pro Ala Met Gly Ser Glu Gly Ala Ala
25                               30                               35

```

## (2) INFORMATION FOR SEQ ID NO: 65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 32..100

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.5

seq LTFLQLLLISSLP/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGTAGACGCT CGGGCACCAG CMGCGGCAAG G ATG GAG CTG GGT TGC TGG ACG	52
Met Glu Leu Gly Cys Trp Thr	
-20	
CAG TTG GGG CTC ACT TTT CTT CAG CTC CTT CTC ATC TCG TCC TTG CCA	100
Gln Leu Gly Leu Thr Phe Leu Gln Leu Leu Leu Ile Ser Ser Leu Pro	
-15 -10 -5	
AGA GAG TAC ACA GTC ATT AAT GAA GCC TGC CCT GGA GCA GAG TGG AMT	148
Arg Glu Tyr Thr Val Ile Asn Glu Ala Cys Pro Gly Ala Glu Trp Xaa	
1 5 10 15	
ATC ATG TGT CGG GAG TGC TGT GAA TAT GAT CAG ATT GAG TGC GTC TGC	196
Ile Met Cys Arg Glu Cys Cys Glu Tyr Asp Gln Ile Glu Cys Val Cys	
20 25 30	
CCC GGA AAG AGG GAA GTC GTG GGT TAT ACC ATC CCT TGC TGC AGG AAT	244
Pro Gly Lys Arg Glu Val Val Gly Tyr Thr Ile Pro Cys Cys Arg Asn	
35 40 45	
GAG GMG AAT GAG TGT GAC TCC TGC CTG ATC CAC CCA GGT TGT ACC ATC	292
Glu Xaa Asn Glu Cys Asp Ser Cys Leu Ile His Pro Gly Cys Thr Ile	
50 55 60	
TTT GAA AAC TGC AMG ACC TGC CGM AAT GGC TCA TGG GGG GGT ACC TTG	340
Phe Glu Asn Cys Xaa Ser Cys Arg Asn Gly Ser Trp Gly Gly Thr Leu	
65 70 75 80	

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 112..192  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.2  
 seq SLLFFLLLEGGXT/EQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```

AAGACCTCGG AACGAGAGCG CCCCAGGGAG CTGGAGCGGC GTGCACGCGT GGCACACGGA    60
GAAGGCVAKK RCNNNNRCTT GAAGGTTCTG TCACCTTTTG CAGTGGTCCA A ATG AGA    117
                                     Met Arg
RAA AAG TGG AAA ATG GGA GGC ATG AAA TAC ATC TTT TCG TTG TTG TTC    165
Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe
-25                      -20                      -15                      -10
TTT CTT TTG CTA GAA GGA GGC KAA ACA GAG CAA GTR AMN CAT TCA GAG    213
Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His Ser Glu
                      -5                      1                      5
ACA TAT TGC ATG TTT CAA GAC AAG AAG TAC AGA GTG GGT GAG AGA TGG    261
Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp
                      10                      15                      20
CAT CCT TAC CTG GAA CCT TAT GGG TTG GTT TAC TGC GTG AAC TGC ATC    309
His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile
                      25                      30                      35
TGC TCA GAG RAT GGG AAT GTG CTT TGC AGC CGA GTC AGA TGT            351
Cys Ser Glu Xaa Gly Asn Val Leu Cys Ser Arg Val Arg Cys
40                      45                      50

```

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 310 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 62..124  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.2  
 seq VSIMLLLVTVSDC/AV

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

AAAGGCTGAG CCGGAGGAAG CGAGAGGCAT CTAAGCAGGC AGTGTTTTGG CTCACCCCA    60

```

```

AGTGACC ATG ASA GGT GCC ACG CGA GTC TCA ATC ATG CTC CTC CTA GTA    109
      Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val
                -15                      -10

ACT GTG TCT GAC TGT GCT GTG ATC ACA GGG GCC TGT GAG CGG GAT GTC    157
Thr Val Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val
      -5                1                5                10

CAG TGT GGG GCA GGC ACC TGC TGT GCC ATC AGC CTG TGG CTT CGA GGG    205
Gln Cys Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly
                15                20                25

CTG CGG ATG TGC ACC CCG CTG GGG CGG GAA GGC GAG GAG TGC CAC CCC    253
Leu Arg Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro
                30                35                40

GGC AGC CAC AAG ATC CCC TTC TTC AGG AAA CGC AAG CAC CAC ACC TGT    301
Gly Ser His Lys Ile Pro Phe Phe Arg Lys Arg Lys His His Thr Cys
      45                50                55

CCT TGC TTG                                310
Pro Cys Leu
      60

```

## (2) INFORMATION FOR SEQ ID NO: 63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 240..302
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq SALLFSLICEAST/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

ACCTTTCTGG ACCTTGCAAA CTGTGACATA TAAAGCTGT TAGCTGCTCC TCTAGCCAGC    60
AGCATTCAAA CATTGCAGAG CTTTGCTCTC AGAGASTTTG TAAAAGACA CACTCCTCTT   120
ACAAGAGTTC ATGCTACCAC ATAGCAAAGA ACCTTAAATT TTTGGAGAGAA CAATATATTC   180
ATTTTGGCAT TGTGCAGAGC AAGTAAACT CGGTGGCCTC TTCTTCTCCA CCCCTCAAR    239
ATG ATA GCR ATC TCT GCC GTC AGC AGT GCA CTC CTG TTC TCC CTT CTC    287
Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu

```



-20	-15	-10	
TGT GAA GCA AGT ACC GTC GTC CTA CTC AAT TCC ACT GAC TCA TCC CCG	335		
Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro			
-5 1 5 10			
CSA ACC AAT AAT TTC RCT GAT AWT GAA GCA GCT CTG AAA GCA CAT	380		
Xaa Thr Asn Asn Phe Xaa Asp Xaa Glu Ala Ala Leu Lys Ala His			
15 20 25			

## (2) INFORMATION FOR SEQ ID NO: 69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 181..243
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq SALLFSLCEAST/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AGCATTCAAA CCTTGCAGAG CTTTGCTCTC AGAGAGTTTC TAAAAGACA CACTCCTCTT	60
ACAAGAGTTC ATGCTACCAC ATAGCAAAGA ACCTTAAATT TTTGGAAGAA CAATATATTC	120
MATTTTGGCA TTGTGCAGAG CAAAGTAAAC TCGGTGGCCT CTTCTTCTCC ACCCCTCAAA	180
ATG ATA GCA ATC TCT GCC GTC AGC AGT GCA CTC CTG TTC TCC CTT CTC	228
Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu	
-20 -15 -10	
TGT GAA GCA AGT ACC GTC GTC CTA CTC AAT TCC ACT GAC TCA TCC CCG	276
Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro	
-5 1 5 10	
CCA ACC AAT AAT TTC ACT GAT ATT GAA GCA GCT CTG AAA GCA CAA TTA	324
Pro Thr Asn Asn Phe Thr Asp Ile Glu Ala Ala Leu Lys Ala Gln Leu	
15 20 25	
GAT TCA GCG GAT ATC CCC AAA GCC AGG CGG AAG CGC TAC ATT TCG CAG	372
Asp Ser Ala Asp Ile Pro Lys Ala Arg Arg Lys Arg Tyr Ile Ser Gln	
30 35 40	
AAT GAC ATG ATC GCC ATT GTT GAT TAT CAT AAT CAA GTT CGG GGC AAA	420
Asn Asp Met Ile Ala Ile Leu Asp Tyr His Asn Gln Val Arg Gly Lys	
45 50 55	

GTG TTC CCA MCG GCA  
Val Phe Pro Xaa Ala  
60

435

## (2) INFORMATION FOR SEQ ID NO: 70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 352..417
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq LLTLVLCVAVAYE/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```

ATTGAGCTGT CTGCAGCAGA GCTGAGAGGA CCAGCCATTT TACTTATGGA AAACAGTGTG   60
GCATATTCTG CTGAGCTTCG CCCTGGAAGA AGCCTCTTTT ATACATCTCT TCAGGGAAGA   120
GAGAAGCAAT GGGCATGTTA GTATACAATG ATCACAGCCA CGCAGGCCTG CAAGCTGCCT   180
TTTGGACAGG CTSTTGACTG CCGTTC CAAT TAGCTGATTG GAGAAATGTGG AATGCAGACT   240
GATAATGCTG CATATCTGCT ATCAGGCAGC AGCAAAGGTT TTTGTCTTGG GAAGGCAAGC   300
TTTCCCTGCA ATATTATCTC AGCAGCTCCC TAGCTGCTTA CCCTGAAAAC G ATG GAT   357
                                     Met Asp
CCA AAC GGA GGG TGT TGC ACT CTG CTA ACG CTG GTC CTG TGC GTG GCT   405
Pro Asn Gly Gly Cys Cys Thr Leu Leu Thr Leu Val Leu Cys Val Ala
-20          -15          -10          -5

GTG GCA TAT GAG CGG CAG GAG   426
Val Ala Tyr Glu Arg Gln Glu
1

```

## (2) INFORMATION FOR SEQ ID NO: 71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 288..362  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.2  
 seq LFTFSTSLPSSLS/SS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```

ACAATACCTG TTACTTATAT ACTTTTCTTT GTCTAAAAAA GAAATAAGAT CTGTCTAGAT   60
GACTGATTAA CTTAGGGAGA TTCTGATTAA CAGAATTCTT AGAAATGGCT TTCAGCAGGC   120
AAAGASAAAA TTATATTTTG TACCAATTTA TATAAAGTTC ATCTAGCTCA GCTTTTGGAG   180
ATGTCCCTGG GGCTAGAGAT GAAATATCGT TTTCTGTCC ACAGACAGCG GTCTGCAGTT   240
CACCCCATGA ACTCATACAG GTCAGAATTA AACCCCGAGC TTTGTTT ATG GAG GGT   296
                                   Met Glu Gly
                                   -25

GAG ATA TAT TTC CAA GTA TTT CTT TCT CTT TTC ACA TTT TCC ACA TCA   344
Glu Ile Tyr Phe Gln Val Phe Leu Ser Leu Phe Thr Phe Ser Thr Ser
   -20               -15               -10

TTA CCA TCA TCA TTG TCG TCA TCA TCA TTG TCA TCA TCC AAT GGG   389
Leu Pro Ser Ser Leu Ser Ser Ser Ser Leu Ser Ser Ser Asn Gly
   -5               1               5

```

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 328 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 194..316  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7  
 seq FLCMLAIDLALS/TS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

ATGAGTCAGC CTGAAAGGAA CAGGCCGAAC TGCTGTATGG GCTCTACTGC CASTGTGACC 60
TCACCCCTCTC CAGTCACCCC TCCTCAGTTC CAGCTATGAG TTCCTGCAAC TTCACACATG 120
CCACCTTTGT GCTTAATKGG AATCCCAGGG ATTAGAGAAA GCCCATTCTT GGGTTGGCTT 180
CCCCCTCCTT TCC ATG TAT GTA GTG GCA ATG TTT GGA AAC TCC ATC GTG 229
      Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val
      -40 -35 -30
GTC TTC ATC GTA AGG ACG GAA CGC AGC CTG CAC GCT CCG ATG TAC CTC 277
Val Phe Ile Val Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu
      -25 -20 -15
TTT CTC TGC ATG CTT GCA GCC ATT GAC CTG GCC TTA TCC ACA TCC ACC 325
Phe Leu Cys Met Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr
      -10 -5 1
ATG 328
Met

```

## (2) INFORMATION FOR SEQ ID NO: 73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 79..207
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq PWFLAPWCPGTQS/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

ACGCTTCGTT CTGGTTCTGG TTCTAGTTCT GGTCTAACA ACTCACAATC CCTTTAGCTT 60
TCTCTCCCTT CCCTTTGA ATG AGA GAA ACT AMC CCG CTT CCG AAG CCC CTG 111
      Met Arg Glu Thr Xaa Pro Leu Pro Lys Pro Leu
      -40 -35
AAA GAC ACT GCT CCT TCC TCT CAT GGA GTT GGC TCC GAC AGC CCG TCT 159
Lys Asp Thr Ala Pro Ser Ser His Gly Val Gly Ser Asp Ser Pro Ser
      -30 -25 -20
GCC ACC AGG CCA TGG TTC CTT GCC CCA TGG TGT CCT GGG ACC CAG AGC 207
Ala Thr Arg Pro Trp Phe Leu Ala Pro Trp Cys Pro Gly Thr Gln Ser

```



Val Pro Gly

## (2) INFORMATION FOR SEQ ID NO: 75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 3..65
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq VILLFSYPSCCLC/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

AT ATG CAT TAT TTT GTT GCT GGG AAA GTA ATC CTT CTC TTC TCT TAT	47
Met His Tyr Phe Val Ala Gly Lys Val Ile Leu Leu Phe Ser Tyr	
-20 -15 -10	
CCA TCA TGT TGT TTG TGT TTC TTG GTG TAC AGG AGA GTA AGC WAT TTA	95
Pro Ser Cys Cys Leu Cys Phe Leu Val Tyr Arg Arg Val Ser Xaa Leu	
-5 1 5 10	
TTT AAG TGC TTT GAG	110
Phe Lys Cys Phe Glu	
15	

## (2) INFORMATION FOR SEQ ID NO: 76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 160..216
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7

seq STVVLQVLTQATS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

ACACGCCCARA CATGGCGTGT TCCTAGAAGC CGCTTTCGGC ATCAGTAGGC GGCGGGGTGG	60
GGTGTGGCAK CGTGGGGAGA GGGAMCAACC GACGCCACTT CGTGTGTGCA ACTCGGAGCG	120
GGANRGCCCG GCAATTCCCG ACCGAACCAA ACGGTTTCC ATG GAT CTC AAT AGT	174
Met Asp Leu Asn Ser	
-15	
GCC AGC ACT GTT GTT CTT CAG GTG TTA ACA CAG GCC ACC AGT CAG GAT	222
Ala Ser Thr Val Val Leu Gln Val Leu Thr Gln Ala Thr Ser Gln Asp	
-10 -5 1	
ACT GCT GTG TTA AAA CCA GCT GAG GAG CAG TTG AAG CAG TGG GAG ACA	270
Thr Ala Val Leu Lys Pro Ala Glu Glu Gln Leu Lys Gln Trp Glu Thr	
5 10 15	
CAG CCA GGW TTC TAT TCA GTG TTG CTG AAT ATT TTC ACC AAC CAC GGG	318
Gln Pro Gly Phe Tyr Ser Val Leu Leu Asn Ile Phe Thr Asn His Gly	
20 25 30	

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 95..313  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7  
seq FLCMLAAIDLALS/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

ATGAGTCAGC CTGAAAGAAC AGGCCGAAC TCTGTATGGG CTCTACTGCC AGTGTGACCT 60  
CACCCCTCTCC AGTCACCCCT CCTCAGTTCC AGCT ATG AGT TCC TGC AAC TTC ACA 115  
Met Ser Ser Cys Asn Phe Thr  
-70  
CAT GCC ACC TTT GTG CTT ATT GGT ATC CCA GGA TTA GAG AAA GGC CAT 163  
His Ala Thr Phe Val Leu Ile Gly Ile Pro Gly Leu Gln Lys Ala His  
-65 -60 -55

```

TTC TGG GTT GGC TTC CCC CTC CTT TCC ATG TAT GTA GTG GCA ATG TTT      211
Phe Trp Val Gly Phe Pro Leu Leu Ser Met Tyr Val Val Ala Met Phe
-50                      -45                      -40                      -35

GGA AAC TGC ATC GTG GTC TTC ATC GTA AGG ACG GAA CGC AGC CTG CAC      259
Gly Asn Cys Ile Val Val Phe Ile Val Arg Thr Glu Arg Ser Leu His
                      -30                      -25                      -20

GCT CCG ATG TAC CTC TTT CTC TGC ATG CTT GCA GCC ATT GAC CTG GCC      307
Ala Pro Met Tyr Leu Phe Leu Cys Met Leu Ala Ala Ile Asp Leu Ala
                      -15                      -10                      -5

TTA TCC ACA TCC ACC ATG                                          325
Leu Ser Thr Ser Thr Met
      1

```

## (2) INFORMATION FOR SEQ ID NO: 78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 179..346
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq PLFFSCSISATHS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```

ACAAAATCAA GAAATCCAA CATAGATGGT CAAAATATTC ATAGGTGACT GAGASTATCC      60
AAATGGGCCA GGTGACTGAG AATACGCAAA CAGGCCAGAA TAATATCTGT GTTAAATTTG      120
ACCTCTATT TTATTAACAT ATCTGTCATG ACCTTTCTCT GTACCTGCTG TAGTACTC      178
ATG TAT AGA CTC AGT CTT ATA GCA GGC CCT GGG TCC TAT CCT GTG CTA      226
Met Tyr Arg Leu Ser Leu Ile Ala Gly Pro Gly Ser Tyr Pro Val Leu
-55                      -50                      -45

AGA TGG GGA GTT TGG GAC ATC CCT AGT TCA TTA GTT CAA GTG ACT TAC      274
Arg Trp Gly Val Trp Asp Ile Pro Ser Ser Leu Val Gln Val Thr Tyr
-40                      -35                      -30                      -25

CAT CAG CCC AAC CTC ACT ACA AAT TTG GAT CTG CCT TTG TTC TTC AGT      322
His Gln Pro Asn Leu Thr Thr Asn Leu Asp Leu Pro Leu Phe Phe Ser
      20                      -15                      -10

TGT AGT ATC TCG GCT ACC CAT TCT TGT GTC AAG CCT CCA TCT GTA ATT      370

```





## (2) INFORMATION FOR SEQ ID NO: 80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 33..137
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq XLXXLLTPPPSYG/HQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

AACCGGCCCCG CGCCCCGCCA TGGAGGACCT GG ATG CCC TGC TCT CTG ACC TGG      53
                               Met Pro Cys Ser Leu Thr Trp
                               -35                               -30

AGA CTA CCA CCT CGC ACA TGC CAA KGT CAK GGG CTY CYA AAG AGC GYY      101
Arg Leu Pro Pro Arg Thr Cys Gln Xaa Xaa Gly Leu Xaa Lys Ser Xaa
      -25                               -20                               -15

CTT GYG GAB CTK CTC ACC CCT CCC CCA TCC TAT GGC CAC CAG CCA CAG      149
Leu Xaa Xaa Leu Leu Thr Pro Pro Pro Ser Tyr Gly His Gln Pro Gln
      -10                               -5                               1

ACA GGG TCT GGG GAG TCT DCA GGA GCC TCG GGG GAC AAG GAC CAC CTG      197
Thr Gly Ser Gly Glu Ser Xaa Gly Ala Ser Gly Asp Lys Asp His Leu
      5                               10                               15                               20

TAC AGC ACG GTA TGC                                          212
Tyr Ser Thr Val Cys
      25

```

## (2) INFORMATION FOR SEQ ID NO: 81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 15..137
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8  
seq LFLFLTSLAEXCS/TP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

```

ACCCTGTKCT TKTC ATG GTT DTC TGG CTC GTC TTA TTT GCT CTT CAG ATT      50
      Met Val Xaa Trp Leu Val Leu Phe Ala Leu Gln Ile
      -40                      -35                      -30

TAC TCC TAT KKY AGT ACT CGA GAT CAG CCT GCA TCA CGT GAK AGG CTT      98
Tyr Ser Tyr Xaa Ser Thr Arg Asp Gln Pro Ala Ser Arg Xaa Arg Leu
      -25                      -20                      -15

CTT TTC CTT TTT CTG ACA AGT ATT GCG GAA TRC TGC AGC ACT CCT TAC      146
Leu Phe Leu Phe Leu Thr Ser Ile Ala Glu Xaa Cys Ser Thr Pro Tyr
      -10                      -5                      1

TCT CTT TTG GGT TTK GTC TTC ACG GTT TCT TTT GTT GCC TTG GGT GTT      194
Ser Leu Leu Gly Xaa Val Phe Thr Val Ser Phe Val Ala Leu Gly Val
      5                      10                      15

CTC ACA CTC TGC AAG TTT TAC TTG CAG GGT TAT CGA GCT TTC ATG AAT      242
Leu Thr Leu Cys Lys Phe Tyr Leu Gln Gly Tyr Arg Ala Phe Met Asn
      20                      25                      30                      35

GAT CCT GCC ATG AAT CGG GGA GGT GCG                                  269
Asp Pro Ala Met Asn Arg Gly Gly Ala
      40

```

## (2) INFORMATION FOR SEQ ID NO: 82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 9..62
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq LPLLXXXSLPVGA/WL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

AAGTCCTG ATG GCC CGG CAT GGG TTA CCG CTG CTG CHB YWG HTG TCG CTC 50  
 Met Ala Arg His Gly Leu Pro Leu Leu Xaa Xaa Xaa Ser Leu  
 -15 -10 -5

CCG GTC GGC GCG TGG CTC 68  
 Pro Val Gly Ala Trp Leu  
 1

## (2) INFORMATION FOR SEQ ID NO: 83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 258..368
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq ILYILWYCSVCSS/GS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

AAGGTTGGTC TGGACCGGAA GCGAAGATGG CGACTTCTGG CGCGGCCTCG GCGGASTGGT 60  
 GATCGGCTGG TGCATATTCG GCCTCTTACT ACTGGCKATT TTGGCATTCT GCTGGATATA 120  
 TSTTCGTAAG TACCAAAGTC GCGCGGAAAG TGAAGTTGTC TCCACCATAA CAGCAATTTT 180  
 TTCTCTAGCA ATTGCACTTA TCACATCAGC ACTTCTACCA GTGGATATAT TTTTGGTTTC 240  
 TTACATGAAA AATCAAAA ATG GTA CAT TTA AGG ACT GGG CTA ATG CTA ATG 290  
 Met Val His Leu Arg Thr Gly Leu Met Leu Met  
 -35 -30  
 TCA GCA GAC AGA TTG AGG ACA CTG TAT TAT ACG GTT ACT ATA CTT TAT 338  
 Ser Ala Asp Arg Leu Arg Thr Leu Tyr Tyr Thr Val Thr Ile Leu Tyr  
 -25 -20 -15  
 ATT CTG TGG TAT TGT TCT CTG TGT TCT TCT GGA TCC CTT TTG TCT ACT 386  
 Ile Leu Trp Tyr Cys Ser Val Cys Ser Ser Gly Ser Leu Leu Ser Thr  
 -10 -5 1 5  
 TCT ATT ATG AAG AAA AGG ATG 407  
 Ser Ile Met Lys Lys Arg Met  
 10

## (2) INFORMATION FOR SEQ ID NO: 84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 196..240
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq ILSTVTALTFFARA/LD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```

AAAAAATTGG TCCAGTTTT CACCCGTCCG CAGGGCTGGC TGGGGAGGGC AGCGGTTTAC   60
ATTAGCCGTG GCCTAGGCCG TTAAACGGGG TGACACGAGC HTGCAGGGCC GAGTCCAAGG  120
CCCGGAGATA GCACCAACCG TCAGGAATGC GAGGAATGTT TTTCTTCGGA CTCTATCGAG  180
GCACACAGAC AGACC ATG GGG ATT CTG TCT ACA GTG ACA GCB TTA ACA TTT   231
      Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
      -15                -10                -5

GCC AGA GCC CTG GAC GGC TGC AGA AAT GGC ATT GCC CAC CCT GCA AGT   279
Ala Arg Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
      1                5                10

GAG AAG CAC AGA CTC GAG AAA TGT AGG GAA CTC GAG AGC AGC CAC TCG   327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser
      15                20                25

GCC CCA-GGA TCA ACC CAG CAG                                     348
Ala Pro Gly Ser Thr Gln Gln
      30                35

```

## (2) INFORMATION FOR SEQ ID NO: 85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 45..113  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.5  
 seq LTFLQXLLISSLX/RE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

ACTCTCCCTC CCCASTAGAC GCTCGGGCAC CAGCCGCGGC AAGG ATG GAG CTG GGT      56
                               Met Glu Leu Gly
                               -20

TGC TGG ACG CAG TTG GGG CTC ACT TTT CTT CAG STC CTT CTC ATC TCG      104
Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Xaa Leu Leu Ile Ser
      -15                      -10                      -5

TCC TTG CHA AGA GAG TAC ACA GTC ATT AAT GAA GCH CGC AAG      146
Ser Leu Xaa Arg Glu Tyr Thr Val Ile Asn Glu Ala Arg Lys
      1                      5                      10

```

## (2) INFORMATION FOR SEQ ID NO: 86:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (E) TISSUE TYPE: Prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 201..266  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.4  
 seq FLLCXSVFTDCKG/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

ACAGAATCAC GTTTTDAGTT GTGCGTGTGC GCGCACACGM GTGTAAAMAG CACTTTCGAT      60

TGTGCCTCCT GTTTTCTCGA GTGGGGACAC TTAACTACA GTTTASACCT CGGGCGCATM      120

AAGTTTKTCT TCTCTTTCTC TCTGTTTIT TCTGTTTCTG AGTGGACCAA CAGCAGARCC      180

CACGAGGAKT TGTTTTGAGT ATG GAG CTG TTG CGG GTD TGC TCC TTT TTC TTG      233
      Met Glu Leu Leu Arg Val Cys Ser Phe Phe Leu
      -20                      -15

CTT TGC TSC TCA GTT TTT ACA SAC TGT AAA GGA GAT GTG TTG TGT GTG      281
Leu Cys Xaa Ser Val Phe Thr Asp Cys Lys Gly Asp Val Leu Cys Val
      -10                      -5                      1                      5

```

AAG ATG GAG CAG AGT CAA ATC TGT GCT  
 Lys Met Glu Gln Ser Gln Ile Cys Ala  
 10

308

## (2) INFORMATION FOR SEQ ID NO: 87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 203..268
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq TWFLLLPPGQCRA/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AGAATCTCAC GAGAGAAGAA AACCAGCCAC ATAAAGGATT TGAAAGCTCA ACTTGCTTTC 60  
 CCACTCTGTT ATCCCTGGAG TTGGCTTGA TTCACCTGA AGCCTTCCCC CTCCCGGGGA 120  
 AAGTTGCTTC ACGTTGCAGC TCAGCAGSTT TGTCCAGCTA CATAGGCTCC AGAAAACAAG 180  
 AAGCAAGACT GGAAAGCTGG GG ATG ATT GTA CGC CCT CGC CTG AAT CTT ACG 232  
                   Met Ile Val Arg Pro Arg Leu Asn Leu Thr  
                   -20                                  -15  
 TGG TTC CTC CTT CTT CCA CCT GGC CAG TGC AGA GCC GTG GGT GCC ACG 280  
 Trp Phe Leu Leu Leu Pro Pro Gly Gln Cys Arg Ala Val Gly Ala Thr  
                   -10                                  -5                                  1  
 TGG CCC GGG 289  
 Trp Pro Gly  
                   5

## (2) INFORMATION FOR SEQ ID NO: 88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..57  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq MVALCCCLWKISG/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```

ATG CAA TTC TTG TTT AAG ATG GTG GCC TTA TGC TGT TGT CTC TGG AAG      48
Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu Trp Lys
      -15                      -10                      -5

ATC TCC GGC TGT GAG GAA GTC CCT CTA ACT TAC AAC CTG CTC AAG TGC      96
Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu Lys Cys
      1                      5                      10

CTC CTA GAT AAA GCG CAC GTA GGG                                      120
Leu Leu Asp Lys Ala His Val Gly
      15                      20

```

## (2) INFORMATION FOR SEQ ID NO: 89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 50..112  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq CVCAAAXXSQSLX/XX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

AAAGCGTCCT ATCCGGAGCC AACTGTAGCT GGCATCCAGE GAGAGGAAG ATG CTC AAG      58
                                Met Leu Lys
                                -20

GTG TCA GCC GTA CTG TGT GTG TGT GCA GCC GCT TDG TGS AGT CAG TCT      106
Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Xaa Xaa Ser Gln Ser
      -15                      -10                      -5

CTC GGM RCT KCC GCG GCG GTG GCT GCA GCC GGS GGG CGG TCG GAC GGC      154

```



Leu Xaa Xaa Xaa Ala Ala Val Ala Ala Ala Gly Gly Arg Ser Asp Gly  
                   1                                  5                                  10

GGT AAT TTT CTG GAT GAT AAA CAA TGG CTC ACC ASR ATC TCT CAG TAT      202  
 Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Xaa Ile Ser Gln Tyr  
   15                                  20                                  25                                  30

GAC AAG GAA KTC GGM MAG TGG AAC AAA TTC CGA GAC GAT KAT TAT      247  
 Asp Lys Glu Xaa Gly Xaa Trp Asn Lys Phe Arg Asp Asp Xaa Tyr  
                                   35                                  40                                  45

## (2) INFORMATION FOR SEQ ID NO: 90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 124..186
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
                                   seq MVALCCCLWKISG/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

AAGACGCTGC CTTTAGGGAG AGATAAAAAG CATAATGACA TTAGCTAGGA AAGTTAATTT      60

TCAGTTCTTA CTGAAGTGCT GTATGAAACT GAAATTTCCA AGGAACTGAA TTTTGTGAGC   120

CAA ATG AGC ATG CAA TTC TTG TTT AAG ATG GTG GCC TTA TGC TGT TGT      168  
 Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys  
   -20                                  -15                                  -10

CTC TGG AAG ATC TCC GGC TGT GAG GAA GTC CCT CTA ACT TAC AAC CTG      216  
 Leu Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu  
   -5                                  1                                  5                                  10

CTC AAG TGC CTC CTA GAT AAA GCG CAC TGT GTA CTC CTG ACA CCT TGT      264  
 Leu Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys  
                                   15                                  20                                  25

GGT TAC ATC TTT TCC TTG ATC AGT CCA GGG      294  
 Gly Tyr Ile Phe Ser Leu Ile Ser Pro Gly  
                                   30                                  35

## (2) INFORMATION FOR SEQ ID NO: 91:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 114..164
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq LWILLGSLSCRTS/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```
AATTCTTATA GGIGTGTCCA GCAGGCAGTG GCTTGTAGCT GTTCCITCAG CCACTTAACA    60
GGTTTGATTT CAAAGCTTTT TAATAGAGAA ACTAACATGT TTGCAGGGGA TTC ATG      116
                                         Met
GCC CAA CAT TTA TGG ATT TTG TTG GGA AGT CTC AGT TGC CGA ACA AGC      164
Ala Gln His Leu Trp Ile Leu Leu Gly Ser Leu Ser Cys Arg Thr Ser
-15                               -10                               -5
AAC CGG CGG                                173
Asn Arg Arg
1
```

## (2) INFORMATION FOR SEQ ID NO: 92:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 66..149
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq LYLFSGFWTFXLG/KF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

ACACTTGART TGGGGTTAAG TTGAAGAACA GACAACTTA GACACAAAGC TATGCAAAAA   60
TCGTG ATG AAC AAG GAA RAA GTA AGT TTN GAA AGG ARA GCA CAG GTC AGA   110
    Met Asn Lys Glu Xaa Val Ser Xaa Glu Arg Xaa Ala Gln Val Arg
          -25                -20                -15

TTA TAT TTA TTC TCA GGA TTT TGG ACT TTT KTA TTA GGG AAA TTT AAA   158
Leu Tyr Leu Phe Ser Gly Phe Trp Thr Phe Xaa Leu Gly Lys Phe Lys
          -10                -5                1

CAA GGG GAA TGR TCT TAT ATK KGT ATT CTA GAA AGA TTA CTG TGG CAG   206
Gln Gly Glu Xaa Ser Tyr Xaa Xaa Ile Leu Glu Arg Leu Leu Trp Gln
          5                10                15

CAG CAG TAT GWA GGA TGG CTT GTA GGR GAT AAG AGA   242
Gln Gln Tyr Xaa Gly Trp Leu Val Gly Asp Lys Arg
    20                25                30

```

## (2) INFORMATION FOR SEQ ID NO: 93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 200..361
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq IVFIFLILLNTAA/QV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

ATTGAAAGAT GGTAAPATGG TGCAGAAGGG GACTTACACT GAGTTCCTAA AATCTGGTAT   60
AGATTTTGGC TCCCTTTTAA AGAAGGATAA TGAGGAAGT GAACACCTC CAGTTCCAGG   120
AACTCCCAACA MYAAGGGAAT CGTACCCTTC TCAGAGTCTT CGCTTTGGTC TCAACAATCT   180
TCTAGACCCT CCTTGAAAG ATG GTG CTC TGG AGA GCC AAG ATA CAN MGG AAT   232
    Met Val Leu Trp Arg Ala Lys Ile Xaa Arg Asn
          -50                -45

GTC CCA GTT ACA CTA TCA GAG GAG AAC CGT TCT GAA SGA AAA GTT GGT   280
Val Pro Val Thr Leu Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly
          -40                -35                -30

TTT CAG GCC TAT AAG AAT TAC TTC AGA GCT GGT GCT CAC TGG ATT GTC   328
Phe Gln Ala Tyr Lys Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val
          -25                -20                -15

```

```

TTC ATT TTC CTT ATT CTC CTA AAC ACT GCA GCT CAG GTT GCC TAT GTG      376
Phe Ile Phe Leu Ile Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val
   -10                      -5                      1                      5

CTT CAA GAT TGG TGG CTT TCA TAC TGG GCA AAC AAA CAA AGT ATG CTA      424
Leu Gln Asp Trp Trp Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu
               10                      15                      20

AAT GTC ACT GTA AAT                                          439
Asn Val Thr Val Asn
               25

```

## (2) INFORMATION FOR SEQ ID NO: 94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 125..178
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq FTSVLWLTSPSQP/NT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

ATGTAGTGAA TAAAGTTTGA GAACCACTGA CTTGAACTTT AGCATGATTT GATACACAGG      60
GTCCCTCTGTA ATCGTACTTC GTTCTGCTTT AAGGCTGTTG GGCTGTCTCC TCCAACCCAT      120
CCKK ATG TTG TTG TAK TTT TTC ACC TCK GTC CTT TGG CTT ACG TCA CCN      169
Met Leu Leu Xaa Phe Phe Thr Ser Val Leu Trp Leu Thr Ser Pro
               -15                      -10                      -5

TCC CAA CCT AAT ACC TGC CCT TCT AGT CTT CTG TGT ACT TAT CCA AAT      217
Ser Gln Pro Asn Thr Cys Pro Ser Ser Leu Leu Cys Thr Tyr Pro Asn
               1                      5                      10

CTA AAC CCT CCA TGG                                          232
Leu Asn Pro Pro Trp
               15

```

## (2) INFORMATION FOR SEQ ID NO: 95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs

(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 140..205  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq IILGCLALFLLQ/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```
AACAGTTACG AAGGAGAGCT GCAAAAGTTG CAGCAGAAAG GTTGGGAGTC CCGACAGGTT    60
CCGTAGCCCA CAGAAAAGAA GCAAGGGACG GCAGGACTGT TTCACATTT TCTGCTTCTG    120
GAAGGTGCTG GACAAAAAC ATG GAA CTA ATT TCC CCA ACA GTG ATT ATA ATC    172
           Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
           -20                               -15
CTG GGT TGC CTT GCT CTG TTC TTA CTC CTT CAG CGG AAG AAT TTG CGC    220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
-10                               -5                               1                               5
AGA CCC TGG    229
Arg Pro Trp
```

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 134..274  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq TWLGLLSFQNLHC/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

ATCATTTTCT TATCCCTGCT GATTTCAAAC CTTCCTCATGG TTATGAAACA TAACTGTAA 60
TGTAAATGCAA GTCCCTAAC TCCCTGGTTG CTAACATTAA CTTCCTTAAG TAATAATCAA 120
TGAAAGAVAT TCT ATG CAT GST TTT GAA ATA ATA TCC TTT AAA GAG GAA 169
      Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu
      -45 -40
TCA CCA TTA GGA AAG GTG AGT CAG GGT CCT TTG TTT AAT GTG ACT AGT 217
Ser Pro Leu Gly Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser
-35 -30 -25 -20
GGC TCA TCA TCA CCA GTG ACC TGG TTG GGC CTA CTC TCC TTC CAG AAC 265
Gly Ser Ser Ser Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn
-15 -10 -5
CTG CAT TGC TTC CCA GAC CTC CCC GGG 292
Leu His Cys Phe Pro Asp Leu Pro Gly
      1 5

```

## (2) INFORMATION FOR SEQ ID NO: 97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 270..437
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq NTLFLHLSGLSAA/DT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```

AAGCTCTGAG ACAGGAGCCC AGCCCTGGGA TTTTCAGGTG TTTTCATTTG GTGGTCAGGC 60
CTGAACAGAG TGTTTTCTTT TGGTGGTCAG GACTGAGCAG AGAGACCTCA CCATGGAGCT 120
TKGGSYGKTG CKGGCTTTTT CTGTGGCCA TTTTGAAAGA TGTCGGGTCT GAGGGACAAC 180
TATTGGAATC TGGGGGAAGT TCGGTCCAGC CCGGGGAGTC CCTGGGACTC TCCTGTGCAG 240
CCGCTGGATT CCGNTTTCGC AATTTTGGC ATG ACT TGG GTC CGC CAC GCT CCA 293
      Met Thr Trp Val Arg His Ala Pro
      -55 -50
GGG AAG AGT CTG GAA TGG GTC GCA ACC GTC ACA GAT GGT GST GAT AAG 341
Gly Lys Ser Leu Glu Trp Val Ala Thr Val Thr Asp Gly Gly Asp Lys
-45 -40 -35

```

```

ACC TTT TAT GCG GCC TCC GTG AAG GGC CGC TTC AAC GTC TCC AGG GAC      389
Thr Phe Tyr Ala Ala Ser Val Lys Gly Arg Phe Asn Val Ser Arg Asp
      -30                -25                -20

AAT TCC AAG AAC ACG TTA TTT CTG CAT TTG AGC GGC CTG AGT GCC GGC      437
Asn Ser Lys Asn Thr Leu Phe Leu His Leu Ser Gly Leu Ser Ala Ala
      -15                -10                -5

GAC ACC GGC TGG TGG GGG ATC                                          458
Asp Thr Gly Trp Trp Gly Ile
      1                5

```

## (2) INFORMATION FOR SEQ ID NO: 98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 143..184
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq LTSFFSLTANCQS/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

AACATACCCT TCAGGTTTAG GTCTTTCTTA GGTAAAGTTT TAACTTTAGT ATATCTTCCT      60
CAGGGCGGCC TTCTCCTTCC CCCTAGTAAG TGRAGAAACC CTTGTGKTG TGCCTCTGA      120
ACTCACCACA TTTGGGATTA CC ATG CTA ACA TCC TTT TTT TCA CTG ACT GCA      172
          Met Leu Thr Ser Phe Phe Ser Leu Thr Ala
                      -10                -5

AAT TGC CAG AGT GCA GGA ACT ATC TCA TTT GCT GCT TTC TCC CTA ATG      220
Asn Cys Gln Ser Ala Gly Thr Ile Ser Phe Ala Ala Phe Ser Leu Met
          1                5                10

CCT GGA                                          226
Pro Gly

```

## (2) INFORMATION FOR SEQ ID NO: 99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 72..125  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.8  
seq LTPLFFMXPTGFS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```
ACTTCCCTTC CCCCTCTAGC ATTGCTACCT TCTCTCTAC ACGCACGCAG SCATATAAAC    60
GTAGGTITTT G ATG CTC CTC TGC CTG TTG ACC CCG CTA TTT TTC ATG TTK    110
              Met Leu Leu Cys Leu Leu Thr Pro Leu Phe Phe Met Xaa
              -15                               -10
CCA ACA GGT TTT TCT TCC CCC AGT CCT GGG                                140
Pro Thr Gly Phe Ser Ser Pro Ser Pro Gly
-5                               1                               5
```

(2) INFORMATION FOR SEQ ID NO: 100:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 178..240  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq HSLFLSLLGLCPS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```
AATGGCGCG GGCCTCCGT AGCCACGGCA ACAGGTGCT TGTGAGTCT GAGCTGAGCG    60
CCTTTCGCAC GACTTGGAGT TACGGTTTAT TTGATACCCC GGTACCCCTA CGCAAGCAAG    120
CCCACATCGA CACACATTCA CACACGCCCT TCAGCACCCC CTCCCAGCAC CACGACC      177
```



G TTC TTG TCG CTC CTC 225  
 u Phe Leu Ser Leu Leu  
 -10

A AAT GGT CCC GTC TTT 273  
 u Asn Ala Pro Val Phe  
 10

288

prostate

Heijne matrix  
 5.7  
 VWLLLGHMVVS/QM

0: 101:

G TCCCAATTAT ACCCGGTTGG 60

A AATCTTCSTA CCCATTTTGC 120

C TCGTGCCAA GGAGCCATGC 180

T AGGCTTCCAC TTCTATTCCT 240

T TTGAGTGGAG CTTCTGG 297

T CTC CTT GGC CAC ATG 345

u Leu Leu Gly His Met  
 -5

A AAG CAC AGA CCC TGG 393

g Lys His Arg Pro Trp  
 10

- (A) LENGTH: 281 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 135..251
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq LTQGVWLWILVIQA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

ATATACAGAG AATAACGTC ATCCCTCTAA CATTAAATATG TTCAGTTTTA TGTACCTGAG    60
AGTTGATGGT TTAATTTGTG GGTTCGCCCA GACTCTCTTG CGACTTCTCT CATCATCTGC   120
TCTTTAGCAC TTCC ATG AGA CGG GGC AAG AGA TTG TTG GAG TCT CAA TCC    170
      Met Arg Arg Gly Lys Arg Leu Leu Glu Ser Gln Ser
                        -35                               -30
AGC AGC CCG AAA GCC TGT CTG CAG CTT GGG TTT GAG ACT GAA CTA ACT    218
Ser Ser Pro Lys Ala Cys Leu Gln Leu Gly Phe Glu Thr Glu Leu Thr
      -25                               -20                               -15
CAG GGT GTT TTG TGG ATT TTA GTT ATC CAG GCT GTC CCT GTT CCC TCA    266
Gln Gly Val Leu Trp Ile Leu Val Ile Gln Ala Val Pro Val Pro Ser
      -10                               -5                               1                               5
TTA ACA AAA ACA AAA                                                281
Leu Thr Lys Thr Lys
                        10

```

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 205..264
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7  
seq ALLESVVWLPCHG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

AGACCAGGCG CATTTCCTCAG AAGCCTTTGG CTCCCCTGAG ATGCCAAATA GCGGCTCACT   60
CTTCCGCCTC CACGSACTGG CTTTGGTGTT CATGCTGGTT GGGATGTCTA CTATGGACCT   120
GCTGASCACA GGCCTGGCTT CCTGGGGCAC AGAGTTGATG CTTATGGCCC AGGAACIGCT   180
GGGCCCCAGG ACTGGGCGGT TTCC ATG GTT GCT GCC ACA GAA GCA GCA TTG   231
                        Met Val Ala Ala Thr Glu Ala Ala Leu
                        -20                      -15

CTG GAG TCA GTA GTG TGG CTG CCT TGC CAT GGC CGT GGT GGG TCT   276
Leu Glu Ser Val Val Trp Leu Pro Cys His Gly Arg Gly Gly Ser
-10                      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 356..412
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq VSLPLLSSWGSTA/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

AATTACAGCT CTACAATGCA CCAGACGGAC CCATCTGGAT TCTTTCGGGG CTCTTAGCCC   60
TAGAAATAGC ATCATTTCCT CAAACTGGTG AGTCCTCCTG TCTAAAATCA GGATGCAGAG   120
AGTTGATGCA CGGCATGGCA CAGGATGCTG GGCAAGGCTG GCAGGCCCGG GAGAGCCTGT   180
GSCCAGCCTG GGTCCAGGAA GTGGGCAGCT GCCACAGAGG GGCCTCCGAG GCTAGCTGCC   240
TCTTAACTTC CTCACGGCAC ACCAATCTGC CGTCCTGAGT CTTCTCAAGG TTGGAAGGTG   300
CCCAGATCCA GGGAGATGGT GCTGGCTCTT TGSTGGCTGT GGAGTGTCCA GACAG ATG   358
                        Met

AGC TGG AAT CCT TCA GTT TCT CTG CCT CTC CTG TCA AGT TGG GGT AGC   405
Ser Trp Asn Pro Ser Val Ser Leu Pro Leu Leu Ser Ser Trp Gly Ser

```

-15

-10

-5

ACT GCT TGG ACT CTT  
 Thr Ala Trp Thr Leu  
 1

421

## (2) INFORMATION FOR SEQ ID NO: 105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 53..118
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq LILLSLHLERRWT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

ACAATAATAA CTAATGAGAT TAAAATTTAA AACAGSTGTC TGATAATCCT TG ATG AAG 58  
 Met Lys

AGA ATT CAG GGG ATA TTG TTC CTG ATT TTG CTT TCT CTC CAC TTG GAA 106  
 Arg Ile Gln Gly Ile Leu Phe Leu Ile Leu Leu Ser Leu His Leu Glu  
 -20 -15 -10 -5

AGG AGG TGG ACC AGC CCA TCA GAC CAC AGC CTG TTG CTA GGA GGA AAT 154  
 Arg Arg Trp Thr Ser Pro Ser Asp His Ser Leu Leu Leu Gly Gly Asn  
 1 5 10

TCC TTG GCT CAA CAT GCA GAA AGT GTA GTA CGC CAA GGG 193  
 Ser Leu Ala Gln His Ala Glu Ser Val Val Arg Gln Gly  
 15 20 25

## (2) INFORMATION FOR SEQ ID NO: 106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 298..402  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.5  
 seq LLTFGLEVCLAAG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

AAAGGAAGGG GGGGCGGAAC CAGCCTGCAC GCGCTGGCTC CGGGTGACAG CCGGCGGCGT   60
CGGCCAGGAT CTGAGTGATG AGACGTGTCC CCACTGAGGT GCCCCACAGC AGCAGGTGTT   120
GAGCATGGGC TGAGAAGCTG GACCGGCACC AAAGGGCTGG CAGAAATDVG CGCCTGGCTG   180
ATTCTAGGC AGTTGGCRGC AGCAAGGAGG AGAGGCCGCA GCTTCTGGAG CAGAGCCGAG   240
ACGAAGCAGT TCTGGAGTGC CTGAACGGCC CCCTGAGCCC TACCGGCCTG GCCCACT   297
ATG GTC CAG AGG CTG TGG GTG AGC CGC CTG CTG CGG CAC CGG AAA GCC   345
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
-35                -30                -25                -20

CAG CTC KKG CTG GKC AAC CTC CTA ACC TTT GGC CTG GAG GTG TGT TTG   393
Gln Leu Xaa Leu Xaa Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
-15                -10                -5

GCC GCA GGA TCA CCT ATG TGC CGC CTC TGC TGC TGG AAG TGG   435
Ala Ala Gly Ser Pro Met Cys Arg Leu Cys Cys Trp Lys Trp
      1                5                10
  
```

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 27..80  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.5  
 seq PFALVTSCSSVFS/GD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

AGACGGAACC AGCTGCGGAG CGCACT ATG GCT GCT GGC GTA CCC TTT GCG TTA   53
  
```

Met Ala Ala Gly Val Pro Phe Ala Leu  
-15 -10

GTC ACC ACC TGC TCC TCC GTC TTC TCA GGA GAC CAG CTG GTC CAA CAT 101  
Val Thr Ser Cys Ser Ser Val Phe Ser Gly Asp Gln Leu Val Gln His  
-5 1 5

ATC CTT GGA ACA GAA GAT CTT ATT GTG GAA GTG ACT TCT AAT GAT GCT 149  
Ile Leu Gly Thr Glu Asp Leu Ile Val Glu Val Thr Ser Asn Asp Ala  
10 15 20

GTG AGA TTT TAT CCC TGG ACC ATT GAT AAT AAA TAC TAT TCA GCA GAC 197  
Val Arg Phe Tyr Pro Trp Thr Ile Asp Asn Lys Tyr Tyr Ser Ala Asp  
25 30 35

ATC AAT CTA TGT GTG GTG CCW AAC AAA TTT CTT GTT ACT GCA GAG ATT 245  
Ile Asn Leu Cys Val Val Pro Asn Lys Phe Leu Val Thr Ala Glu Ile  
40 45 50 55

GCA GAA TCT GTC CAA GCA TTT GTG GTT TAC TTT GAC DKC ACA CAA RAA 293  
Ala Glu Ser Val Gln Ala Phe Val Val Tyr Phe Asp Xaa Thr Gln Xaa  
60 65 70

TCG GGC CTT GAT AGT GTC TCC TCA TGG CTT CCA CTG GCA AAA GCA TGG 341  
Ser Gly Leu Asp Ser Val Ser Ser Trp Leu Pro Leu Ala Lys Ala Trp  
75 80 85

TTA CCT GAG GTG ATG ATC TTG GTC TGC GAT AGA GTG TCT GAA GAT GGT 389  
Leu Pro Glu Val Met Ile Leu Val Cys Asp Arg Val Ser Glu Asp Gly  
90 95 100

ATA 392  
Ile

## (2) INFORMATION FOR SEQ ID NO: 108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 290..331
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq TVFLXFCFPRCHS/DS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

AATGCTGAAC GGWCACACAG AGAGGAAACW ATAAATKKYA GCTACTATGC AATAAATATC 60

```

TCAGCTTTTA ACGAAGAAAA ACATCATTCG AGTGAAATAA AAAATTTTAA AATTTTAGAA 120
CAAAGCTAAC AAATGGCTAG TTTTCTATGN TTCTTCTTCA AACGCTTTCT TTGAGGGGRM 180
AAGAGTCAMA CAAACAAGCA GTTTTACCTA AAATAAAGAA CTAGTTTTAG AGGTCAGAMG 240
AMAGSMGCAA GTTTTGCGAG WGGCACGGAA GGAGTGTGCT GGCAGTACA ATG ACA GTT 298
                               Met Thr Val
TTC CTT TMN TTT TGC TTT CCT CGC TGC CAT TCT GAC TCA CAT ARG RTG 346
Phe Leu Xaa Phe Cys Phe Pro Arg Cys His Ser Asp Ser His Xaa Xaa
-10                               -5                               1                               5
CAG CAA TCA GCG 358
Gln Gln Ser Ala

```

## (2) INFORMATION FOR SEQ ID NO: 109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 44..187
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq ILLEVFVWNLQG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```

AATTCTTCC TGCCAAGAGA ACAATGCCGA GAAACAGAGC GAA ATG KTT CCA AAT 55
                               Met Xaa Pro Asn
                               -45
AAT TTT TGG CAA AAA CTT GGA AGA AAA AAA CCC CGC ATA TTT ACC TGT 103
Asn Phe Trp Gln Lys Leu Gly Arg Lys Lys Pro Arg Ile Phe Thr Cys
-40                               -35                               -30
ACC CAG AGC TCC ACA GGT GAG GCG GCA GTT AAA GCA GAA AAT CTA ATT 151
Thr Gln Ser Ser Thr Gly Glu Ala Ala Val Lys Ala Glu Asn Leu Ile
-25                               -20                               -15
CTT CTG GAA GTT TTT GTC TGG AAC GGA CTC CAG GGT CTT CCT TCG GAG 199
Leu Leu Glu Val Phe Val Trp Asn Gly Leu Gln Gly Leu Pro Ser Glu
-10                               -5                               1
CTG TCA GAT ACA AGT GGA TCC TCT AAG AAA CTT GGG AGC CTT GTG GGC 247
Leu Ser Asp Thr Ser Gly Ser Ser Lys Lys Leu Gly Ser Leu Val Gly

```

5	10	15	20	
TGG TGG AGA ACT CTC AAG ATG GCA CCA GCC TGT CTA TGG TCT ATG TGG	295			
Trp Trp Arg Thr Leu Lys Met Ala Pro Ala Cys Leu Trp Ser Met Trp				
25 30 35				
GAA TCA CCG CCA CGG	310			
Glu Ser Pro Pro Arg				
40				

## (2) INFORMATION FOR SEQ ID NO: 110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 66..173
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq ALYIMCVPHSVWG/CA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

AAGTCCAGAG GCCTGGCCCT GCCAAGAAGG CGCTCTCCGG AATCAACACC TGGGGGCTTG	60
GAAGG ATG TTT CGC TCA GAT CGA ATG TGG ARC TGC CAT TGG AAA TGG AAG	110
Met Phe Arg Ser Asp Arg Met Trp Xaa Cys His Trp Lys Trp Lys	
-35 -30 -25	
CCC AGT CCT CTC CTG TTC TTA TTT GCT TTA TAT ATC ATG TGT GTT CCT	159
Pro Ser Pro Leu Leu Phe Leu Phe Ala Leu Tyr Ile Met Cys Val Pro	
-20 -15 -10	
CAC TCA GTG TGG GGA TGT GCC AAC TGC CGA GTG GTT TTG TCC AAC CCT	206
His Ser Val Trp Gly Cys Ala Asn Cys Arg Val Val Leu Ser Asn Pro	
-5 1 5 10	
TCT GGG ACC TTT ACT TCT CCA TGC TAC CCT AAC GAC TAC CCA AAC AGC	254
Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser	
15 20 25	
CAG GCT TGC ATG TGG ACG CTC CGA GAC CCC	284
Gln Ala Cys Met Trp Thr Leu Arg Asp Pro	
30 35	

## (2) INFORMATION FOR SEQ ID NO: 111:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 123..215
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq LVALSSELPLGA/GV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

TCCTTCATCT TGTGTTCTAA AACCTTGCAA GTTCAGGAAG AAACCATCTG CATCCATATT      60
GAAAACCTGA CACAATGTAT GCAGCAGGCT CAGTGTGAGT GAACTGGAGG CTTCTCTACA      120
AC ATG ACC CAA AGG AGC ATT GCA GGT CCT ATT TGC AAC CTG AAG TTT      167
  Met Thr Gln Arg Ser Ile Ala Gly Pro Ile Cys Asn Leu Lys Phe
    -30                -25                -20

GTG ACT CTC CTG GTT GCC TTA AGT TCA GAA CTC CCA TTC CTG GGA GCT      215
Val Thr Leu Leu Val Ala Leu Ser Ser Glu Leu Pro Phe Leu Gly Ala
  -15                -10                -5

GGA GTA CAG CTT CAA GAC AAT GGG TAT AAT GGA TTG CTC ATT GCA ATT      263
Gly Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile
   1                 5                 10                15

AAT CCT CAG GTA CCT GAG AAT CAG AAC CTC ATC TCA AAC ATT AAG GAA      311
Asn Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu
    -                20                25                30

ATG ATA ACT GAA GCT TCA TTT TAC CTA TTT AAT GCT ACC AAG AGA AGA      359
Met Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg
    35                40                45

GTA TTT TTC AGA AAT ATA AAG ATT TTA ATA CCT GCC CAG      398
Val Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Gln
   50                55                60

```

## (2) INFORMATION FOR SEQ ID NO: 112:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 187..228  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.3  
seq IIPLLLLLRSACN/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

ACTCCAGGAG CCGGGACCAA AATAACCGGG CGGGAGGGGA CACCTCGCAG AGATGGATCT   60
CGAACTCCTG GGCTCAAGCG ATCCTTTCAC CTTGGCCTCT CAAGTAGCTG GGACCACATT  120
TGCTCACCAG CTGGCCCAAG ACCAGACTGG GCAACATGGG TCATCCTCCT CTAAGATTCC  180
AGGACC ATG ATC ATC CCT CTA TTG CTA CTT CTT AGA TCA GCT TGT AAT   228
      Met Ile Ile Pro Leu Leu Leu Leu Arg Ser Ala Cys Asn
                -10                      -5

GTC CAT CTC CCC CAC CAG ACT GCG TCT CCA GCA TCT CTG AGT CCC CAG   276
Val His Leu Pro His Gln Thr Ala Ser Pro Ala Ser Leu Ser Pro Gln
  1              5              10              15

GGC CTG GCC TGG GGC TTG CTA CAT GGT GGG TGC TCA GTA ACT GTG AGA   324
Gly Leu Ala Trp Gly Leu Leu His Gly Gly Cys Ser Val Thr Val Arg
      20              25              30

```

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 231..287  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.3  
seq VLLLSXNLNLIQ/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

ACTATGGAGG GAAGACACAG GGAAAGGAGT ATTTCAAAAA CTTAAATAA TTGTACATAA   60

```

TTGGAGCAAG TGAGAAGACA AGTKAGAGGT AAGGNGKTRT TGAGAATAGG GGKCTGATTG 120  
 TGCCAGCTTT GTATACVATT ATNAGGAACN DGGACTTGTG CCTGAAGGTA ACTGGGCAAT 180  
 TGTGAGGTC ACCACCATCT ACTGTCTGGA TTAACGAGGA AACTTTCTAA ATG TMS 236  
 Met Xaa  
 TCT CCA CTT CCA GTC CTG CTC CTC TCA TGC AAT CTC AAC CTA ATA ATT 284  
 Ser Pro Leu Pro Val Leu Leu Leu Ser Xaa Asn Leu Asn Leu Ile Ile  
 -15 -10 -5  
 CAG AGT AGT 293  
 Gln Ser Ser  
 1

## (2) INFORMATION FOR SEQ ID NO: 114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 244..381
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LLTFLVFTXKLSS/LN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

ACACTGAAAT CAATCTGTTC AATAGCAITTA TACCATATTT GACATACCAT AGCCATGTTA 60  
 ATCTGATATT GTAGAATAGC ATAGTAKAAT AATAATAACT CCTAACTCAA GGATGTTGWG 120  
 WKCCTTTATA ACCAGCAATC CATGTTARAT ATTAGCACAG TGCCTAAAAC ATATTAAGCA 180  
 TTCAATAAAT GATCGCTACT ATTTTACTA ACATCCTACA GATTTGGAAA TTGACTCTTA 240  
 GAA ATG TTA ATG TGT AAA ATG CTA AAG AGC CAA AAA AAC TGC CAG GAA 288  
 Met Leu Met Cys Lys Met Leu Lys Ser Gln Lys Asn Cys Gln Glu  
 -45 -40 -35  
 AAT ATR ARA ATT AAA ATC ATT TTA TTT CTG AAA CCC ATG TGT TCC CCC 336  
 Asn Xaa Xaa Ile Lys Ile Ile Leu Phe Leu Lys Pro Met Cys Ser Pro  
 -30 -25 -20  
 CAA TAT CTT CTA ACA TTT CTA GTA TTT ACA GRA AAA CTT TCA AGT CTC 384  
 Gln Tyr Leu Leu Thr Phe Leu Val Phe Thr Xaa Lys Leu Ser Ser Leu  
 -15 -10 -5 1

AAU AUC RGA AAG TTT CAT  
 Asn Ile Xaa Lys Phe His  
 5

402

## (2) INFORMATION FOR SEQ ID NO: 115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 306..461
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq IIVILHCAASIIS/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

AAGTATTAAA TTAAAAAGA TAAATCTGCC CTATTCTAAT CATGTCTTG TCTTCTGTTT    60
ATTCAAGTGT ATTCCATTG CTTTCGGGAA TATTTGGATG TTTTAGAACT AACATTCTGC    120
TTTAATAATC CAAACACRCK AYMAYTYCCA TCAATTTGAG TCTCTTAAAA TGTTACACTG    180
AAATGAATCT CTCTGAAGAT GGAATTATTG ATTTCTATAT TCTTCCTCTA GCATCATGAA    240
ATTTGACCTC TTCAGCCGTG CATGGTTAAC ACTCAGATAA CCCATCTCCT TGAGAAGAAC    300
CCCTG ATG AAR AAG AAA TCC TCT CCA AAT CAA TAT CTT CAT TCA TCA CTA    350
  Met Lys Lys Lys Ser Ser Pro Asn Gln Tyr Leu His Ser Ser Leu
        -50                -45                -40

CAC TRS ATA CGN CTA TTT TCC TTC CTC CAT TTC TCA GAG GAA GGA GTT    398
His Xaa Ile Arg Leu Phe Ser Phe Leu His Phe Ser Glu Glu Gly Val
        -35                -30                -25

CTA TTA CTT GCC ATT GAT CTT AAA ATT ATA GTT ATC CTC CAC TGT GCT    446
Leu Leu Leu Ala Ile Asp Leu Lys Ile Ile Val Ile Leu His Cys Ala
        -20                -15                -10

GCA TCC ATA ATT TCA TGT CCC TCA                                470
Ala Ser Ile Ile Ser Cys Pro Ser
        -5                1

```

## (2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 334 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 116..184  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.1  
 seq ATSVSLEAQSCFA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

ATTTTGAAG ACTGTAATGC TTTAAACTT ACTTTATTGG ATCTCTTTCG AGCTTTTGAC   60
ACASTGAACC ACTTTCCTTT CCTGAAATGC TTTCTCTCTT TGGCTTTCCTG ATGCC ATG   118
                                     Met
TTC TCC TGT TTC TTC TCT ACT TCT CTG GCC ACT TCT GTC TCC TTA GAA   166
Phe Ser Cys Phe Phe Ser Thr Ser Leu Ala Thr Ser Val Ser Leu Glu
      -20                      -15                      -10

GCT CAG TCT TGC TTT GCC TGG CCC TTG ATT GTT AGT TTT CCC CAG GGC   214
Ala Gln Ser Cys Phe Ala Trp Pro Leu Ile Val Ser Phe Pro Gln Gly
      -5                      1                      5                      10

TCA CTT CTT AGC CCC TTT CTC CTC ATG TCT TAT AAT TTG AGT CAT CTC   262
Ser Leu Leu Ser Pro Phe Leu Leu Met Ser Tyr Asn Leu Ser His Leu
              15                      20                      25

ATC TAC TCT GGG GAG TTG AAT GGT CGC TTG TAT GCT GAA AAC TCC CAA   310
Ile Tyr Ser Gly Glu Leu Asn Gly Arg Leu Tyr Ala Glu Asn Ser Gln
              30                      35                      40

ATT TGT ATC TGT AGC CCA GCC GGG   334
Ile Cys Ile Cys Ser Pro Ala Gly
      45                      50
  
```

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 78..227  
 (C) IDENTIFICATION METHOD: Von Heljne matrix  
 (D) OTHER INFORMATION: score 5.1  
 seq RTALILAVQKSSA/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

AGTTTCCAAG GGAAGGAGCA GCGTGTGGGA AAGCACAGAA GAGTGAGAAG GAAGCGACTA    60
AATTTTATTT ACTTTCT ATG CAT CAT GGC CTC ACA CCA CTG TTA CTT GGT    110
      Met His His Gly Leu Thr Pro Leu Leu Leu Gly
      -50                -45                -40

GTA CAT GAG CAA AAA CAG CAA GTG GTG AAA TTT TTA ATC AAG AAA AAA    158
Val His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys
      -35                -30                -25

GCA AAT TTA AAT GCA CTG GAT AGA TAT GGA AGA ACT SCT CTC ATA CTT    206
Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu
      -20                -15                -10

GCT GTA TGT TGT GGA TCG GCA AGT ATA GTC AGC CTT CTA CTT GAG CAA    254
Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln
      -5                1                5

AAC ATT GAT GTA TCT TCT CAA GAT CTA TCT GGA CAG ACG GCC CCC GGG    302
Asn Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Pro Gly
      10                15                20                25
  
```

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 319..369  
 (C) IDENTIFICATION METHOD: Von Heljne matrix  
 (D) OTHER INFORMATION: score 5.1  
 seq IYFFACEQALTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```

AGAGTAGGCG GAGACAGAGA GGCTGTATTT CAGTGCAGCC TGCCAGACCT CTTCTGGAGC    60
  
```

```

AASACTGGAC AAAGGGGGTC ACACATTCCT TCCATACGCT TGACCTCTA CTTGCTGGT 120
GCTGGTCACA GTTCAGCTTC TTCATGATGG TGGATCCCAA TGGJAATGAA TCCASTGCTA 180
CATACTTCAT CCTAATAGGC CTCCTTGTT TAGAAGAGAG TCAATCTGG TTGGCCTTCC 240
CAATGTGCTC CCTCTACCTT ATTGCTGTGC TAGGTAACCT GACAATCATC TACATTGTGC 300
GCAATGAGCA CAGCCTGC ATG AGC CCA TGT ATA TAT TTC TTT GCA TGC TTT 351
Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe
-15 -10

CAG GCA TTG ACA TCC TCA TCT CCA CCT CAG 381
Gln Ala Leu Thr Ser Ser Ser Pro Pro Gln
-5 1

```

## (2) INFORMATION FOR SEQ ID NO: 119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 49..141
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VSGASGFLPPARS/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

CTTTCTGTGT CTCCTTCCT CCGCCTCAGT TTGGGGCGGG TCGGGGGA ATG GCT GAG 57
Met Ala Glu
-30

GAG ATG GAG TCG TCG CTC GAG GCA AGS TTT TCG TCC AGC GGG GCA CTC 105
Glu Met Glu Ser Ser Leu Glu Ala Xaa Phe Ser Ser Ser Gly Ala Val
-25 -20 -15

TCA GGG GCC TCA GGG TTT TTG CCT CCT GCC CGC TCC CGC ATC TTC AAG 153
Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg Ile Phe Lys
-10 -5 1

ATA ATC GTG ATC GGC GAC VBC AAT GTG GGC AAG ACA TGC CTG ACC TAC 201
Ile Ile Val Ile Gly Asp Xaa Asn Val Gly Lys Thr Cys Leu Thr Tyr
5 10 15 20

CGC TTC TGC GCT GGC CGC TTC CCC GAC CGC ACC GAG GCC ACG ATA GGG 249
Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg Thr Glu Ala Thr Ile Gly

```

25	30	35	
GTG GAT TTC CGA GAA CGA GCG GTG GAG ATT GAT GGG GAG CGC ATC AAG			297
Val Asp Phe Arg Glu Arg Ala Val Glu Ile Asp Gly Glu Arg Ile Lys			
40	45	50	
ATC CAG CTA TGG GAC ACA GCA			318
Ile Gln Leu Trp Asp Thr Ala			
55			

## (2) INFORMATION FOR SEQ ID NO: 120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 61..153
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VSGASGFLPPARS/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

AAATCTCTCA GCCTTTCTGT GTCTCCTTTC CTCCGCCTCA GTTGGGGGCG GGTCGGGGGA	60
ATG GCT GAG GAG ATG GAG TCG TCG CTC GAG GCA AGC TTT TCG TCC AGC	108
Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Ser Phe Ser Ser Ser	
-30                      -25                      -20	
GGG GCA GTG TCA GGG GCC TCA GGG TTT TTG CCT CCT GCC CGC TCC CGC	156
Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg	
-15                      -10                      -5                      1	
ATC TTC AAG ATA ATC GTG ATC GGC GAC TCC AAT GTD VGC AAG ACA TGC	204
Ile Phe Lys Ile Ile Val Ile Gly Asp Ser Asn Val Xaa Lys Thr Cys	
5                      10                      15	
CTG ACC TAC CGC TTC TGC GCT GGC CGC TTC CCC GAC CGG	243
Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg	
20                      25                      30	

## (2) INFORMATION FOR SEQ ID NO: 121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: NUCLEIC ACID



(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 153..233  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq HLSLILLKPLCLP/NN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```

ACCTTTTATA AACATTTTGT TTAACTTTTA TTGTGGTAAA ATACACATAA CACTTCTCTT   60
CTTTTAGACC TGGGCTGGTA AGAAGTGCTG AAGATGTTTT TTAGAGATTG GTGGTATGAC   120
AAATTCCACT GGGGTTTCTG ASCTTCTCAG TC ATG CTT GTC TTG GGG TCA CCA   173
                               Met Leu Val Leu Gly Ser Pro
                               -25

CTC CTT GGC CCT CTC CTA TGG CAC CTG TCC CTC ATT CTG CTC AAG CCC   221
Leu Leu Gly Pro Leu Leu Trp His Leu Ser Leu Ile Leu Leu Lys Pro
-20                               -15                               -10                               -5

CTA TGC CTT CCC AAC AAC TTG CCT TTA GCT CTG GGC AGA TGT CTT TGC   269
Leu Cys Leu Pro Asn Asn Leu Pro Leu Ala Leu Gly Arg Cys Leu Cys
                               1                               5                               10

TTG CAC TCG   278
Leu His Ser
15

```

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 56..220  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq VLFMTTAVDLVIT/EV

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

AGAAAGGTGT TTTGGTCTTC TCCTTAGTCC ACGAAAAGAT GTACGAAATA GTGAC ATG      58
                                         Met
                                         -55

CAC TTA TTA GAT TTG GAA TCT ATG GGC AAA AGT TCA GAT GGA AAG TCG      106
His Leu Leu Asp Leu Glu Ser Met Gly Lys Ser Ser Asp Gly Lys Ser
          -50                -45                -40

TAT GTT ATT ACG GGG AGC TGG AAT CCA AAA TCC CCA CAT TTT CAA GTT      154
Tyr Val Ile Thr Gly Ser Trp Asn Pro Lys Ser Pro His Phe Gln Val
          -35                -30                -25

GTA AAT GAA GAA ACT CCT AAA GAT AAA GTC CTG TTT ATG ACC ACA GCT      202
Val Asn Glu Glu Thr Pro Lys Asp Lys Val Leu Phe Met Thr Thr Ala
          -20                -15                -10

GTA GAT TTG GTA ATA ACA GAA GTA CAG GAG CCT GTT CGA TTT CTC CTG      250
Val Asp Leu Val Ile Thr Glu Val Gln Glu Pro Val Arg Phe Leu Leu
          -5                1                5                10

GAG ACA AAA GTC CGC GTT TGC TCA CCT AAT GAA AGA TTA TTC TGG CCC      298
Glu Thr Lys Val Arg Val Cys Ser Pro Asn Glu Arg Leu Phe Trp Pro
          15                20                25

GCG
Ala
                                         301

```

## (2) INFORMATION FOR SEQ ID NO: 123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..63
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq VLFVFSSIPLTFL/FQ

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

ATG GAG AAT TTG AAA GAC TTT TAT GTG TTG TTT GTA TTC TCT AGC ATT      48
Met Glu Asn Leu Lys Asp Phe Tyr Val Leu Phe Val Phe Ser Ser Ile
-20                -15                -10

```

CCC CTT ACA TTT CTA TTT CAG AAA TTG CCT TTT GTT TGG ATT KGA GAA 96  
 Pro Leu Thr Phe Leu Phe Gln Lys Leu Pro Phe Val Trp Ile Xaa Glu  
 -5 1 5 10

GAG ACT TTG GAG ACA TGG TAT TTG AAG AGC TGG 129  
 Glu Thr Leu Glu Thr Trp Tyr Leu Lys Ser Trp  
 15 20

## (2) INFORMATION FOR SEQ ID NO: 124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 293..346
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LSIFSLVLPVCRM/HR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

ACAAITCCAG CTTATGTGTC CCTTTTATAA ACTGTGATA CATTTTAACT STGTATACAC 60  
 ATCTCTTGCC TCTATTGGTA GAGAGTATCT GSCAKGCCTA GCATGTGCTG GATGTCATAT 120  
 CAGATACTCA GTGTTATTTA TTGGGCTTAC AGTGATAACC AAAGCTCACA TGTTTATGCA 180  
 CTCCCACTTC CATAAAGTGG AAGATGTCCC CTCTGCCTCT TCTCTCATCC CTCCTCAAAG 240  
 CAGCAGGAGT GACTTACCTG ATTGACCACT TTAAGACTAT ATCTGAGCAG GC ATG CCA 298  
 Met Pro

CAG TAC TGT CTC AGC ATC TTC TCT CTT GTG CTG CCT GTC TGC AGG ATG 346  
 Gln Tyr Cys Leu Ser Ile Phe Ser Leu Val Leu Pro Val Cys Arg Met  
 -15 -10 -5

CAG AGG 352  
 His Arg  
 1

## (2) INFORMATION FOR SEQ ID NO: 125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 15..143

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8  
seq LLAFGTSCSVVLY/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```

GACCAGTTGG CGAC ATG GTG GCA CCC GTG CTG GAG ACT TCT CAC GTG TTT      50
      Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe
                        -40                      -35

TGC TGC CCA AAC CGG GTG CGG GGA GTC CTG AAC TGG AGC TCT GGG CCC      98
Cys Cys Pro Asn Arg Val Arg Gly Val Leu Asn Trp Ser Ser Gly Pro
-30                      -25                      -20

AGA GGA CTT CTG GCC TTT GGC ACG TCC TGC TCC GTG GTG CTC TAT GAC     146
Arg Gly Leu Leu Ala Phe Gly Thr Ser Cys Ser Val Val Leu Tyr Asp
-15                      -10                      -5                      1

CCC CTG GGT TGT TGT TAC CAA CTT GAA TGG TCA CAC CGC CCG TTC CGG     194
Pro Leu Gly Cys Cys Tyr Gln Leu Glu Trp Ser His Arg Pro Phe Arg
      5                      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 126:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 134..247

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8  
seq LSWLITWFGHXLS/DF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```

ATTGTGGTCA CATTCTGCT GGTGGTAGGC GAGAGGCTGG CAACATCCCT GGTAGAAAAA      60

```

```

TTATCTACCC ACCACCTCAG GCATTTTATG GATCCAVCAA TGGRACAACA CCAMSCATAT 120
ATTAAACIAT CTG ATG CCC ATC ATT GAC CAG GTG AAT CCA GAG CTC CAT 169
      Met Pro Ile Ile Asp Gln Val Asn Pro Glu Leu His
      -35 -30

GAC TTC ATG CAG AGT GCT GAG GTA GGG ACC ATC TTT GCC CTC AGC TGG 217
Asp Phe Met Gln Ser Ala Glu Val Gly Thr Ile Phe Ala Leu Ser Trp
-25 -20 -15

CTC ATC ACC TGG TTT GGG CAT GWM CTG TCT GAC TTC AGG CAC GTC GTG 265
Leu Ile Thr Trp Phe Gly His Xaa Leu Ser Asp Phe Arg His Val Val
-10 -5 1 5

CGG TTA TAT GAC TTC TTC CTR GCC TGC CAC CCA CTG ATG CCG ATT TAC 313
Arg Leu Tyr Asp Phe Phe Leu Ala Cys His Pro Leu Met Pro Ile Tyr
10 15 20

TTT GCA GCC GTG ATT GTG TTG TAT CGC GAG CAG 346
Phe Ala Ala Val Ile Val Leu Tyr Arg Glu Gln
25 30

```

## (2) INFORMATION FOR SEQ ID NO: 127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 63..209
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq GLCVLVPCXSXX/WR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

AAATKKKKKG ACCATTTCTT TCCCTGACAG CCGGACCTGG KACTGGGCTG GGGCCCTGGC 60
GG ATG GAG ACA TKC TGC CCC TGC TGC TGC TGC CCC TGC KGT GGG GDN 107
      Met Glu Thr Xaa Cys Pro Cys Cys Cys Cys Pro Cys Xaa Gly Xaa
      -45 -40 -35

GGG TCC CTG CAG GAG AAG CCA GTC TAC GAG CTG CAA GTG CAG AAG TCG 155
Gly Ser Leu Xaa Xaa Lys Pro Val Tyr Glu Leu Gln Val Gln Lys Ser
-30 -25 -20

GTG ACG GTG GAG GAG GGC CTG TGC GTC CTT GTG CCC TSC TCC TKC TCT 203
Val Thr Val Gln Glu Gly Leu Cys Val Leu Val Pro Cys Ser Xaa Ser

```

-15	-10	-5	
TAS SCC TGG AGA TCC TGG TAT TCC TCT CCC CCA CTC TAC GTC TAC TGG			251
Xaa Xaa Trp Arg Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp			
1	5	10	
TTC CGG GAC GGG GAG ATC CCA TAC TAC GCT GAG GTT GTG GCC ACA AAC			299
Phe Arg Asp Gly Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn			
15	20	25	30
AAC CCA GAC AGA AGA KTG AAG SMD KAK AYY CAK KGG CCG ATT CCG CCT			347
Asn Pro Asp Arg Arg Xaa Lys Xaa Xaa Xaa Xaa Xaa Pro Ile Pro Pro			
35	40	45	
CCT TGG GGA TGT CCA GAA GAA GAA CTG			374
Pro Trp Gly Cys Pro Glu Glu Glu Leu			
50	55		

## (2) INFORMATION FOR SEQ ID NO: 128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 295..345
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq IYFFACFXLTS/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

ATTTTCAGTG CAGCCTGCCA GACCTCTTCT GGAGGAAGAC TGGACAAAGG GGGTCACACA	60	
TTCCTTCCAT ACGSTTGAGC CTCTACCTGC CTGGTGCTGG TCACASTTCA GCTTCTTCAT	120	
GRWKGGTGGA TCCCAATGGC AATGAATCCA GTGCTACATA CTTCACTCTA ATAGGCCTCC	180	
CTGSTTTAGA AGAGGCTCAG TTCTGGTTGG CCTTCCCATG GTGCTCCCTC TACCTTATTC	240	
CTGTGCTAGG TAACTTGACA ATCATCTACA TTGTGCGGAC TGAGCACAGC CTGC ATG	297	
	Mat	
AGC CCA TGT ATA TAT TTC TTT GCA TGC TTT CAN NNA TTG ACA TCC TCA	345	
Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Xaa Xaa Leu Thr Ser Ser		
-15	-10	-5
TCT CCA CCT CAT CCA TGC CCA AAA TGC TGG CCA TCT TCT GGT TCA ATT	393	
Ser Pro Pro His Pro Cys Pro Lys Cys Trp Pro Ser Ser Gly Ser Ile		

1

5

10

15

CCA CTA  
Pro Leu

399

## (2) INFORMATION FOR SEQ ID NO: 129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 12..92
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq VLKCLSFSXPSLP/GF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

AAGCAACCGG G ATG GGA CGG GGA GAG AGG AGG CAC TAC TGG GGA CCT AAG	50
Met Gly Arg Gly Glu Arg Arg His Tyr Trp Gly Pro Lys	
-25 -20 -15	
CTG GTT CTC AAA TGC CTC TCC TTT TCS SCT CCA AGC CTC CCA GGC TTC	98
Leu Val Leu Lys Cys Leu Ser Phe Ser Xaa Pro Ser Leu Pro Gly Phe	
-10 -5 1	
CTA TGG TCC CTA	110
Leu Trp Ser Leu	
- 5	

## (2) INFORMATION FOR SEQ ID NO: 130:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: 9..164  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
 seq LLAKALHLLKSSC/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```

AGCCTGCG ATG TCT CAA GAT GGC GGA STG GGC GAA TTA AAG CAC ATG GTG      50
Met Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val
      -50                      -45                      -40

ATG AGT TTC CGG GTG TCT GAG CTC CAG GTG CTT CTT GGC TTT GCT GGC      98
Met Ser Phe Arg Val Ser Glu Leu Gln Val Leu Leu Gly Phe Ala Gly
      -35                      -30                      -25

CGG AAC AAG AGT GGA CGG AAG CAC GAG CTC CTG GCC AAG GCT CTG CAC     146
Arg Asn Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His
      -20                      -15                      -10

CTC CTG AAG TCC AGC TGT GCC CCT AGT GTC CAG ATG AAG ATC AAA GAG     194
Leu Leu Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu
      -5                      1                      5                      10

CTT TAC CGA CGA CGC TTT CCC CGG AAG ACC CTG GGG CCC TCT GAT CTC     242
Leu Tyr Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu
      15                      20                      25

TCC CTA AAG                                                                251
Ser Leu Lys
  
```

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 272 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 18..224  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.6  
 seq LGPSLSSLPSALS/LM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

TATTTGGCCC CAAGCCG ATG CAT CAC AGG ATG AAT GAA ATG AAC CTG AGT      50
Met His His Arg Met Asn Glu Met Asn Leu Ser
      -65                      -60
  
```



```

CCA GTG GGG ATG GAG CAG CTG ACT TCA TCC TCT GTG AGC AAT GCC TTG      98
Pro Val Gly Met Glu Gln Leu Thr Ser Ser Ser Val Ser Asn Ala Leu
      -55                      -50                      -45

CCA GTC TCA GGA AGT CAC CTG GGA TTG GCT GCC TCA CCC ACT CAC AGT      146
Pro Val Ser Gly Ser His Leu Gly Leu Ala Ala Ser Pro Thr His Ser
      -40                      -35                      -30

GCC ATC CCT GCC CCA GGC CTC CCA GTG GCA ATT CCA AAC CTG GGT CCC      194
Ala Ile Pro Ala Pro Gly Leu Pro Val Ala Ile Pro Asn Leu Gly Pro
      -25                      -20                      -15

TCC CTG AGC TCT CTG CCT TCT GCT CTG TCT TTA ATG CTA CCA ATG GGT      242
Ser Leu Ser Ser Leu Pro Ser Ala Leu Ser Leu Met Leu Pro Met Gly
      -10                      -5                      1                      5

DTT GGG GAT CGA GGG GTG ATG TGT GGG TTA      272
Xaa Gly Asp Arg Gly Val Met Cys Gly Leu
      10                      15

```

## (2) INFORMATION FOR SEQ ID NO: 132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 62..118
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq IWNLFSLFSTSTT/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

ACATCCTTGA TTCTTTACTT TCTCTTAACA CCTGTATCC AGCTGGTCAT AAATCTAGCA      60
G ATG CTA CAT TCA GAT AAC ATC TGG AAT CTA TTT TCC CTA TTT TCT ACT      109
Met Leu His Ser Asp Asn Ile Trp Asn Leu Phe Ser Leu Phe Ser Thr
      -15                      -10                      -5

TCT ACT ACC CTG CCC CGG      127
Ser Thr Thr Leu Pro Arg
      1

```

## (2) INFORMATION FOR SEQ ID NO: 133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 4..75
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq FHSAAGWSGGGQA/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

ATT ATG CAA CCC GCC TCC CCG CCC GCC CGG TGG AGC TTC CAC TCG GCT      48
Met Gln Pro Ala Ser Pro Pro Ala Arg Trp Ser Phe His Ser Ala
          -20              -15              -10

GCG GGC TGG AGC GGC GGC GGG CAG GCG TGC GGA GGA CAC TCC TGC GAC      96
Ala Gly Trp Ser Gly Gly Gly Gln Ala Cys Gly Gly His Ser Cys Asp
          -5              1              5

CAG GTA CTG GCT GTG ATC GAA CTT CTC AAC CCT CTC AGG      135
Gln Val Leu Ala Val Ile Glu Leu Asn Pro Leu Arg
          10              15              20

```

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 138..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq LLAGSISHMFSQA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```

ATATTTTGGC TTAGCAGCCT GGGCTTCGGA ACTGGGCTTG CCCTGTAGCA GSTCACTTGC      60

```

ACCTTTCTGC CACAGATGAC GGAAACATTT AAAGTTATGG ATTGTGTCTC TGCATCCTCT 120

TCCCTTCACA CCAGCCA ATG TGT TTT TCA TTT CTC TTG GCT GGC TCA ATT 170  
 Met Cys Phe Ser Phe Leu Leu Ala Gly Ser Ile  
 -15 -10

TCC CAC ATG TTC TCC CAA GCT CTT CCG CTC CAC TCC CCA GGG CTT CCC 218  
 Ser His Met Phe Ser Gln Ala Leu Pro Leu His Ser Pro Gly Leu Pro  
 -5 1 5

ACC ACA AAC CGC ACG 233  
 Thr Thr Asn Arg Thr  
 10

## (2) INFORMATION FOR SEQ ID NO: 135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 137..199
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq SILFHCSVCLFLC/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ATATGGCAAG AGATAGAGAT CTAGTTTCAT TCTTCTGCAT ATGGATATCC AATTTTCCCA 60

GCACCATTTA TTGAAGAGAC AGTCCTTTTG CCAGTKTATG TTCTTGGCAA CTTTGTTGAA 120

AATGCATTTA CTGTAG ATG TAT GGA TTC ATT ATT GGG TTA TCT ATT CTG TTC 172  
 Met Tyr Gly Phe Ile Ile Gly Leu Ser Ile Leu Phe  
 -20 -15 -10

CAT TGT TCT GTG TGT CTG TTT TTA TGC CAG TAC CAT GCC TGG 214  
 His Cys Ser Val Cys Leu Phe Leu Cys Gln Tyr His Ala Trp  
 -5 1 5

## (2) INFORMATION FOR SEQ ID NO: 136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 139..210  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.5  
seq SLLGCXLAININT/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```

ATCCTATTGT GTCGTGTAGC TTGTTCTCTA TTTTATAGGT CATTTAAAAT AAAACTCACC   60
TTTGACTTTG ITTAGTCTCT GTTACATGTT TGCITTTTGT TTCGTTTATG TTTGTACATT  120
TCTCATGTKT TTCTKKCT ATG TCT TTT GGT KGT ATT CTA ACT TTT AGA GTC   171
          Met Ser Phe Gly Xaa Ile Leu Thr Phe Arg Val
                               -20                      -15

TCT TTA TTG GGA TGT CNT CTA GCG ATA AAT ATA AAT ACA TTT CCC TCT   219
Ser Leu Leu Gly Cys Xaa Leu Ala Ile Asn Ile Asn Thr Phe Pro Ser
          -10                      -5                      1

AAC AAC CAC TTG   231
Asn Asn His Leu
          5

```

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 12..77  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq LGRLCAGSSGVXG/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

AAAAGCGAGC C ATG GCT GTC TAC GTC GGG ATG CTG CGC CTG GGG AGG CTG   50
          Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu

```

	-20	-15	-10	
TGC GCC GGG AGC TCG GGG GTC STG GGG GCG GCC GSC CTC TCT CGG				98
Cys Ala Gly Ser Ser Gly Val Xaa Gly Ala Arg Ala Xaa Leu Ser Arg				
	-5	1	5	
AGT TGG CAG GAA GCC AGG TTG CAG GGT GTC CGC TTC CTC AGT TCC AGA				146
Ser Trp Gln Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg				
	10	15	20	
GAG GTG GAT CGC ATG GTC TCC ACG CCC ATC GGA GGC CTC ACC TAC GTT				194
Glu Val Asp Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr Val				
	25	30	35	
CAG GGG TGC ACC AAA AAG CAT CTT AAC AGC AAG ACT GTG GGC CAG TGC				242
Gln Gly Cys Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly Gln Cys				
	40	45	50	55
CTG GAG ACC ACA GCA CAG AGG GTC CCG				269
Leu Glu Thr Thr Ala Gln Arg Val Pro				
	60			

## (2) INFORMATION FOR SEQ ID NO: 138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 187..255
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq LVSIFFFWEVTNA/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

AGATAATTTT GATGAAACCA AGAGGCACGT CTTCTACAT ACTTCTCTTC ATCKYCMWTT	60
CCTASTGTTT TNGTTTATKT TTTTAAATA ATGCCCATGT CTCCTGCTGT CATTCTCTGA	120
GACCACCAAA TAGTTTAATA CCTGGAGTCA GAGATAAGAA TAAACAGGCT TAAGATACTT	180
TAAATA ATG TTC AAT ACT ATA TAC TTG GTC ATA TCA TTA GTG AGC ATA	228
Met Phe Asn Thr Ile Tyr Leu Val Ile Ser Leu Val Ser Ile	
	-20 -15 -10
TTT TTC TTT TGG GAA GTA ACT AAT GCT TTC CTT AAG GCC AGG CGT TGG	276
Phe Phe Phe Trp Gln Val Thr Asn Ala Phe Leu Lys Ala Arg Arg Trp	
	-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 36..101
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq SLPLTTGSSWSLS/SQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```
ACCITCTCAA GAACTGTGTT CACCCACTTC CCCAC ATG GCC CTT CCA CCC AAG      53
                               Met Ala Leu Pro Pro Lys
                               -20

GGA TGT GGT AGT CTC CCT TTG ACT ACT GCG TCT TCC TGG AGC CTT TCT      101
Gly Cys Gly Ser Leu Pro Leu Thr Thr Gly Ser Ser Trp Ser Leu Ser
-15                      -10                      -5

TCT CAA ATA GGA AGC CCT GCT ATT TCC AAC CCT AGG      137
Ser Gln Ile Gly Ser Pro Ala Ile Ser Asn Pro Arg
 1                5                10
```

## (2) INFORMATION FOR SEQ ID NO: 140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 44..91
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq FLSWASEFLAPLLR/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

GTCATTGTGC CGTTTCTTCC CCCTTGCCAA TTTTAAATT ASA ATG TTT GTC TTT      55
                               Met Phe Val Phe
                               -15

TTG TCT TGG GCA AGT TTC TTA GCC CCT CTA CTG AGG AGC CCA TTT CTT      103
Leu Ser Trp Ala Ser Phe Leu Ala Pro Leu Leu Arg Ser Pro Phe Leu
-10                               -5                               1

CAT TGT CTA ATG GGG ATG CCA GGG      127
His Cys Leu Met Gly Met Pro Gly
5                               10

```

## (2) INFORMATION FOR SEQ ID NO: 141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 150..233
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq LLSCSPLXPLGKS/GF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```

AAKAGTCAGC AGGAGTKAGT TCAGGAATCC TCGGGACAAG GCACTTTCCT GAGCACTGGA      60

CCAGCGACCT CTTGGCTTCC AGGGAGGACA CACAGCCATC ATGGWACCCA THTCTCAGAA      120

GAGTCCAGGC AAACAGTTTA CATTTTCTT ATG AWA ATG AAG TCT GCA AAC AAG      173
                               Met Xaa Met Lys Ser Ala Asn Lys
                               -25

ATT ACT TTA TTA ART CAC CAC CTT CTC AGC TGT TCT CCT CTG TGW CCT      221
Ile Thr Leu Leu Xaa His His Leu Leu Ser Cys Ser Pro Leu Xaa Pro
-20                               -15                               -10                               -5

CTT GGA AAA AGC GGT TTT TCA TCC TGT CAA AGG CTG GCG AAA AGA GCT      269
Leu Gly Lys Ser Gly Phe Ser Ser Cys Gln Arg Leu Gly Lys Arg Ala
1                               5                               10

TTA GTC TTT CCT ATT ATR AAG NCC ATC ATC ACC      302
Leu Val Phe Pro Ile Xaa Lys Xaa Ile Ile Thr
15                               20

```

12 INFORMATION FOR SEQ ID NO: 142:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 251 base pairs
    (B) TYPE: NUCLEIC ACID
    (C) STRANDEDNESS: DOUBLE
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 150..245
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 4.2
                           seq SFLLLFIVIPQTF/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:
```

|                                         |                                 |                       |     |
|-----------------------------------------|---------------------------------|-----------------------|-----|
| AACTTTGATAA CATCAGCTAA TATTTTTC         | AGTTAGATT                       | TTGAGGTATA ATTTACATAA | 60  |
| GAGTTACTCT TTCTAGAGGT ATAGTTGAAT        | GCATTTTCAC                      | AAATGTGTAC AATTGGATAA | 120 |
| CCACCAMCAT WAWTCTAGAW ATATAGGTA         | ATG TGT AAT TAT AAT ATA TAT GTA |                       | 173 |
|                                         | Met Cys Asn Tyr Asn Ile Tyr Val |                       |     |
|                                         | -30                             | -25                   |     |
| CTA TAT AAT ATA GGA TAT TTA TAC CAC     | CCA AAA AGT TTT CTC TTG CTT     |                       | 221 |
| Leu Tyr Asn Ile Gly Tyr Leu Tyr His     | Pro Lys Ser Phe Leu Leu Leu     |                       |     |
|                                         | -20                             | -15                   | -10 |
| TTT ATA GTC ATT CCC CAA ACC CCA CGT     | CGG                             |                       | 251 |
| Phe Ile Val Ile Pro Gln Thr Pro Arg Pro |                                 |                       |     |
| -                                       | -5                              | 1                     |     |

(2) INFORMATION FOR SEQ ID NO: 143:

- ```
(1) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 383 base pairs
      (B) TYPE: NUCLEIC ACID
      (C) STRANDEDNESS: DOUBLE
      (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo Sapiens
      (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:
      (A) NAME/KEY: sig peptide
```



(B) LOCATION: 84..164  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.2  
 seq PLLAAPLLRSLLP/RX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```

AAGTGAACAG CGGASCGGAC GGGGATCGCC GCGGGCGGCG AAGCGGASGC GGCCACAGGC   60
CCGGCGGTCT CCGAGATGTC ACG ATG GCT GTG GCC ATG GTC AAA CTG TGT GAA   113
                Met Ala Val Ala Met Val Lys Leu Cys Glu
                -25                      -20

AGA GCG GGT CTG CCG CTA CTT GCT GCA CCA CTA CTT AGG TCA CTT CTT   161
Arg Ala Gly Leu Pro Leu Leu Ala Ala Pro Leu Leu Arg Ser Leu Leu
    -15                      -10                      -5

CCA AGA GMA CCT CAG CCT GGA CCA GCT CAG CCT CGA TCT GTA CAA GGG   209
Pro Arg Xaa Pro Gln Pro Gly Pro Ala Gln Pro Arg Ser Val Gln Gly
    1                      5                      10                      15

CAG CGT TGC CCT GCG AGA CAT CCA CCT GGA AAT CTG GTC TGT GAA CGA   257
Gln Arg Cys Pro Ala Arg His Pro Pro Gly Asn Leu Val Cys Glu Arg
                20                      25                      30

GGT GCT RGA GTC AAT GGA GTC ACC GCT GGA GCT RGT GGA ARG CTT CGT   305
Gly Ala Xaa Val Asn Gly Val Thr Ala Gly Ala Xaa Gly Xaa Leu Arg
                35                      40                      45

GGG CTC CAT CGA GGT DGC CGT GCC CTG GGC TGC TCT GCT CAC CGA CCA   353
Gly Leu His Arg Gly Xaa Arg Ala Leu Gly Cys Ser Ala His Arg Pro
    50                      55                      60

MTG CAC AGT GCG CGT GTC CGG CCT CCA GCT   383
Xaa His Ser Ala Arg Val Arg Pro Pro Ala
    65                      70
  
```

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 99..164
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq DVLLGLLKDVLLA/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```

TAAACTTCTG AAAGAAAGAG AAGATCTTCC TATATGGAAA GAAAAATACT CCTTTATGGA    60
GAACTTGCTT CAAAATCAAA TCGTGATTGT TTCAGGAG ATG CTA AAT GTG GTA AGA    116
                               Met Leu Asn Val Val Arg
                               -120

GCG CTC AGG KTY CCT CAG TGG TGT GCT GAA TAT TGT CTT TCC ATC CAC    164
Ala Leu Arg Xaa Pro Gln Trp Cys Ala Glu Tyr Cys Leu Ser Ile His
-115                               -110                               -105

TAC CAG CAC GGG GGC GTG ATA TGC ACA CAG GTC CAC AAG CAG ACT GTG    212
Tyr Gln His Gly Gly Val Ile Cys Thr Gln Val His Lys Gln Thr Val
-100                               -95                               -90                               -85

GTC CAG CTC GCC CTG CGG GTG GCG GAT GAA ATG GAT GTT AAC ATT GGT    260
Val Gln Leu Ala Leu Arg Val Ala Asp Glu Met Asp Val Asn Ile Gly
                               -80                               -75                               -70

CAT GAG GTT GGC TAC GTG ATC CCT TTC GAG AAC TGC TGT ACC AAC GAA    308
His Glu Val Gly Tyr Val Ile Pro Phe Glu Asn Cys Cys Thr Asn Glu
                               -65                               -60                               -55

ACA ATC CTG AGG TAT TGT ACT GAT GAT ATG CTG CAA AGA GAA ATG ATG    356
Thr Ile Leu Arg Tyr Cys Thr Asp Asp Met Leu Gln Arg Glu Met Met
                               -50                               -45                               -40

TCC AAT CCT TTT TTG GGT AGC TAT GGG GTC ATC ATC TTA GAT GAT ATT    404
Ser Asn Pro Phe Leu Gly Ser Tyr Gly Val Ile Ile Leu Asp Asp Ile
-35                               -30                               -25

CAT GAA AGA AGC ATT GCA ACT GAT GTG TTA CTT CGA CTT CTT AAA GAT    452
His Glu Arg Ser Ile Ala Thr Asp Val Leu Leu Gly Leu Leu Lys Asp
-20                               -15                               -10                               -5

GTT TTA CTA GCA AGA CCA GAA CTG AAG                                479
Val Leu Leu Ala Arg Pro Glu Leu Lys
                               1                               5

```

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 107..187
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.2  
seq AGLCIGSTSYVHG/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

ATTGGGAGCA GCAGCATCTA CTTCACAGAC CAGTGTCCAG TTAATTGTGT TTGTGGCAAT   60
CATCCTACAT AAGGCACCAG CTGCTTTTGG ACTGGTTTCC TTCTTG ATG CAT GCT   115
                                     Met His Ala
                                     -25

GGC TTA GAG CGG RAW TCG AWT CAG AAA GCA CTT GCT GST CTT TGC ATT   163
Gly Leu Glu Arg Xaa Ser Xaa Gln Lys Ala Leu Ala Gly Leu Cys Ile
               -20               -15               -10

GGC AGC ACC AGT TAT GTC CAT GGT GAC ATA CTT AGG ACT GAG CGG   208
Gly Ser Thr Ser Tyr Val His Gly Asp Ile Leu Arg Thr Glu Arg
               -5               1               5

```

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 151..255
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq LLGSLSLWRWSAM/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

AATTGCTGGG CTCGAAGCAC AGGAGAGACC AGTCCTTCCT TGTCTCCACT GGGCTGKTAA   60
GTGCTTCTTT CCCAAGGACK TCCATCCCTT CCCAGGCTT TATGGTTCCA GTCCTTCTAC   120
CATTCTGGAA GCTCCCTAGA ATCTCCTGGA ATG CTT AAT GGA CCT TTC CAG CAC   174
                                     Met Leu Asn Gly Pro Phe Gln His
                                     -35               -30

CGA AAT TCA AGA ATT ATG ACT CAT CGG TCA GCA GAA AAG ACC CTG CTG   222
Arg Asn Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys Thr Leu Leu
               -25               -20               -15

GGA TCT TTG AGC TTG TGG AGG TGG TCG GCA ATG GAA COT ACG GAC AGG   270
Gly Ser Leu Ser Leu Trp Arg Trp Ser Ala Met Glu Pro Thr Asp Arg
               -10               -5               1               5

```

TGT ACA AGG GTA GGG  
Cys Thr Arg Val Gly  
10

285

## (2) INFORMATION FOR SEQ ID NO: 147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 44..175
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq IAVGLTCQHVSHA/IS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

AAGGTTGTAG ACGCTGCGGC CCGGCCCGGC GGGTAAATAA CAG ATG CGC GTG AAA	55
Met Arg Val Lys	
GAT CCA ACT AAA GCT TTA CCT GAG AAA GCC AAA AGA AGT AAA AGG CCT	103
Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg Ser Lys Arg Pro	
-40 -35 -30 -25	
ACT GTA CCT CAT GAT GAA GAC TCT TCA GAT GAT ATT GCT GTA GGT TTA	151
Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile Ala Val Gly Leu	
-20 -15 -10	
ACT TGC CAA CAT GTA AGT CAT GCT ATC AGC GTG AAT CAT GTA AAG AGA	199
Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn His Val Lys Arg	
-5 1 5	
GCA ATA GCT GAG AAT CTG TGG TCA GTT TGC TCA GAA TGT TTA AAA GAA	247
Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu Cys Leu Lys Glu	
10 15 20	
AGA AGA TTC TAT GAT GGG CAG CTA GTA CTT ACT TCT GAT ATT TGG TTG	295
Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser Asp Ile Trp Leu	
25 30 35 40	
TGC CTC AAG TGT GGC TTC CAG GGA TGT GGT AAA AAC TCA GAA AGC CAA	343
Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn Ser Glu Ser Gln	
45 50 55	
CAT TCA TTG AAG CAC TTT AAG AGT TCC AGA ACA GAG CCC CAT TGT ATT	391
His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu Pro His Cys Ile	
60 65 70	

ATA ATT AAT CTG AGC ACA  
 Ile Ile Asn Leu Ser Thr  
 75

409

## (2) INFORMATION FOR SEQ ID NO: 148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 184..267
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq ESLLALSMLKGTG/KV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

ACATAATCGG CCTTTATGTT ACACTGCCTG GCCAGCCCCCT GTTATTCTAG TGCATAATTG 60  
 ATGGTGCTCA CAAGTGGAAA AGTTAGAAAA GCGGAAGTAA TGTGACGCAG CAGTGGCATG 120  
 RAGCSCCGG DVCCCCGGCA GTGAGGGCAA TGCAGAGATG GGCTGCTGCT GGCTACCGCC 180  
 AGG ATG CCT CAG AAG GGC CTG GGC TTA CTT GGC ATC TTG TCA GGA GAC 228  
 Met Pro Gln Lys Gly Leu Gly Leu Gly Ile Leu Ser Gly Asp  
 -25 -20 -15  
 TTT TCC CTT CTT GCT TTG TCC ATG CTG AAA GGG ACA GGA AAG GTA GGC 276  
 Phe Ser Leu Leu Ala Leu Ser Met Leu Lys Gly Thr Gly Lys Val Gly  
 -10 -5 1  
 GGG 279  
 Gly

## (2) INFORMATION FOR SEQ ID NO: 149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 69..233  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq AALCGISLSQLFP/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

AAGAACTGA GCAGCCTGTC TTCAGACAGA GAGAGGCCCA CGGCTGTTTC TTGAAAYTGG      60
CGCTGSGA ATG GCC ATG TGG AAC AGG CCA TGB BAG ANG CTG CCT CAG CAG      110
Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln
-55                      -50                      -45

CCT CTS STA GCT GAG CCC ACT GCA GAG GGG GAG CCA CAC CTG CCC ACG      158
Pro Leu Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr
-40                      -35                      -30

GGC CSG GAS BYG ACT GAG GCC AAC CGC TTC GCC TAT GCT GCC CTC TGT      206
Gly Arg Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys
-25                      -20                      -15                      -10

GGC ATC TCC CTG TCC CAG TTA TTT CCT GAA CCC GAA CAC AGC TCC TTC      254
Gly Ile Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe
-5                      1                      5

TGC ACA GAG TTC ATG GCA GGC CTG GTG SKM TGG CTG GAG TTG TCT GAA      302
Cys Thr Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu
10                      15                      20

GCT GTC TTG CCA ACC ATG ACT GCT      326
Ala Val Leu Pro Thr Met Thr Ala
25                      30

```

## (2) INFORMATION FOR SEQ ID NO: 150:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 126..182  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq LLLSPWVTVPVWS/SS

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

CCTACTGCTT AAGGGGATTT AGCATCATCC AAGCAGGGTA AACTTTTGTT TTGTTAAAG   60
AAAAATGTGT TATTCAGTT GGTGTCCCCA GTTGTAAGCTA ACACATCTGG AATGCACCTAA 120
CCAAA ATG CTG TGC TTT GSA GAC CTG CTT TTG TCA CCG TGG GTA ACC GTT 170
      Met Leu Cys Phe Gly Asp Leu Leu Leu Ser Pro Trp Val Thr Val
      -15                -10                -5

CCC GTC TGG TCC AGT AGC CCG TGG   194
Pro Val Trp Ser Ser Ser Pro Trp
      1

```

(2) INFORMATION FOR SEQ ID NO: 151:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 27..107
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq LIYFLGLAATYF/RS

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```

AAGTTAGGTT TAAAGTTTCC TCATTA ATG CAG GAA AAT GCT CAT AAC CTG AGG   53
                        Met Gln Glu Asn Ala His Asn Leu Arg
                        -25                -20

CTT TTC AAG TGT TTA TTA ATT TAC TTT CTG GGG CTG GCT GCT GAT ACT   101
Leu Phe Lys Cys Leu Leu Ile Tyr Phe Leu Gly Leu Ala Ala Asp Thr
      -15                -10                -5

TAT TTC AGA TCA AAG AGA AAG CCT GTG TCT TTC GTA GTT ACT GTG KKG   149
Tyr Phe Arg Ser Lys Arg Lys Pro Val Ser Phe Val Val Thr Val Xaa
      1                5                10

CMA GGA AMC TAT GCC ACA GGG   170
Xaa Gly Xaa Tyr Ala Thr Gly
      15                20

```

(2) INFORMATION FOR SEQ ID NO: 152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 127..303
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq SVATALEFPPLCIS/TG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```

ACCAAGTCCT CCCAAGTTAT TAACTGGTCA AAAAGGMTTA AAGGMTTAGT TCTTAATAGT    60
TAAGATGCCA CCCATTCAGG GTTTTTTGCT TTCTAAGAGG GAACTTTTAC AGGCATAATT    120
GAGAGA ATG CAT ACA TGC TCT CTA CCT TGT CTT CTC TTT GCT CAG CTG      168
      Met His Thr Cys Ser Leu Pro Cys Leu Leu Phe Ala Gln Leu
                        -55                        -50

CTA GAA TTT TGT AGC TTT CCT CCA GAT GTG CCT CAT AAC TGT GCG CCT      216
Leu Glu Phe Cys Ser Phe Pro Pro Asp Val Pro His Asn Cys Ala Pro
-45                        -40                        -35                        -30

ATT GTC TCA GTC AGG CCG CCT AAT ATT GTA GCA GCC TTT GAA GGG TGC      264
Ile Val Ser Val Arg Pro Pro Asn Ile Val Ala Ala Phe Glu Gly Cys
                        -25                        -20                        -15

TCT GTA GCC ACT GCT CTT TTT CCT CCC TTG TGC ATC TCC ACA GGG AAT      312
Ser Val Ala Thr Ala Leu Phe Pro Pro Leu Cys Ile Ser Thr Gly Asn
      -10                        -5                        1

GAG                                                                    315
Glu

```

## (2) INFORMATION FOR SEQ ID NO: 153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate



## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 35..138  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4  
 seq PLLGVLFFQGVYI/VF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```

AGTCGTTACC GGGASCTGTA AACAAAGGTGT GCAAGCATCT GAAGAGCTCC CCGG ATG      57
                                         Met
CAG CAG AGA GGA GCA SCT GGA ACC CGT GGC TGC GCT CTC TTC CCT CTG      105
Gln Gln Arg Gly Ala Ala Gly Ser Arg Gly Cys Ala Leu Phe Pro Leu
      -25                      -20                      -15
CTG GGC GTC CTG TTC TTC CAG GGT GTT TAT ATC GTC TTT TCC TTG GAG      153
Leu Gly Val Leu Phe Phe Gln Gly Val Tyr Ile Val Phe Ser Leu Glu
      -10                      -5                      1                      5
ATT CGT GCA GAT GCC CAT GTC CGA GGT TAT GTT GGA GAA AAG ATC AAG      201
Ile Arg Ala Asp Ala His Val Arg Gly Tyr Val Gly Glu Lys Ile Lys
              10                      15                      20
TTG AAA TGC ACT TTC AAG TCA ACT TCA GAT GTC ACT GAC AAG CTT ACT      249
Leu Lys Cys Thr Phe Lys Ser Thr Ser Asp Val Thr Asp Lys Leu Thr
              25                      30                      35
ATA GAC TGG ACA TAT CGC CCT CCC AGC AGC AGC CAC ACA GTA TCA ATA      297
Ile Asp Trp Thr Tyr Arg Pro Pro Ser Ser Ser His Thr Val Ser Ile
              40                      45                      50
KTK CAT TAT CAG TCT TTC CAG TAC CCA ACC ACA GCA GGC ACA TTT      342
Xaa His Tyr Gln Ser Phe Gln Tyr Pro Thr Thr Ala Gly Thr Phe
              55                      60                      65

```

## (xii) INFORMATION FOR SEQ ID NO: 154:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 109..225  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq LILNRS LPTASSS/SS

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```

AAAAATGTAC TGAATGTCCA CTTTGGGCCA GCCTGGGCAC CGAGGACACA GGGGAACATA   60
GACACAGTCC TGCTCACTGG GAAACTCACA GCCTGTTGGG AAAGAAAG ATG CAM GAV   117
                               Met Xaa Xaa

AGT ATC TTC ATT TCA GAA AAA TAT GGA CTC TGC CCG TCT AAG ACT CCC   165
Ser Ile Phe Ile Ser Glu Lys Tyr Gly Leu Cys Pro Ser Lys Thr Pro
-35                      -30                      -25

ATA ATG AAA ATG CTC CCG TCT TTG ATC CTG AAC CGG TCA TTG CCC ACT   213
Ile Met Lys Met Leu Pro Ser Leu Ile Leu Asn Arg Ser Leu Pro Thr
-20                      -15                      -10                      -5

GCT TCA AGC AGT TCC AGC AGG AAG GAC TTC CGC CTG CCT CAG ACC CGC   261
Ala Ser Ser Ser Ser Ser Arg Lys Asp Phe Arg Leu Pro Gln Thr Arg
                               1                      5                      10

CGG CGA ATC ATC ATG GTG CCT CGC AAG GAG GAT CAG ACA CCC CTT AAT   309
Arg Arg Ile Ile Met Val Pro Arg Lys Glu Asp Gln Thr Pro Leu Asn
15                      20                      25

CCT GCA TCC CAA CCT CAG GCT CCC CCA AAG CCC ATC CCC AGC TTS AAA   357
Pro Ala Ser Gln Pro Gln Ala Pro Pro Lys Pro Ile Pro Ser Xaa Lys
30                      35                      40

AGT YTG GAA GCT AGM GAT AYC AAS RGC AGC CAG AGG ACA BGA AGA CCT   405
Ser Leu Glu Ala Xaa Asp Xaa Xaa Xaa Ser Gln Arg Thr Xaa Arg Pro
45                      50                      55                      60

GGG CTG AGC ACA GGT CGA AGC TGC                               429
Gly Leu Ser Arg Gly Arg Ser Cys
65

```

(2) INFORMATION FOR SEQ ID NO: 155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..350
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 99.1  
region 18..366  
id C83597  
vrt

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 127..186  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq FFWVVLFSAGCKV/IT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```

ATTCTTTGTT CCAAGATCAC CCTTCTGAGT ACCTCTCTGG CTGCCAAATT GCCAGGGCCT    60
TCACASTTTG ATTCCATTTC TCAGCTCCAA GCATTAGGTA AACCCACCAA GCAATCCTAG   120
CCTGTG ATG GCG TTT GAC GTC ASC TGC TTC TTT TGG GTG GTG CTG TTT    180
Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe
-20 -15 -10
TCT GCC GCG TGT AAA GTC ATC ACC TCC TGG GAT CAG ATG TAC ATT GAG    216
Ser Ala Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Tyr Ile Glu
-5 1 5 10
AAA GAA GCC AAC AAA ACA TAT AAC TGT GAA AAT TTA GGT CTC AGT GAA    264
Lys Glu Ala Asn Lys Thr Tyr Asn Cys Glu Asn Leu Gly Leu Ser Glu
15 20 25
ATC CCT GAC ACT CTA CCA AAC ACA ACA GAA TTT TTG GAA TTC AGC TTT    312
Ile Pro Asp Thr Leu Pro Asn Thr Thr Glu Phe Leu Glu Phe Ser Phe
30 35 40
AAT TTT TTG CCT ACA ATT CAC AAT AGA ACC TCC AGC AGG                351
Asn Phe Leu Pro Thr Ile His Asn Arg Thr Ser Ser Arg
45 50 55

```

## (2) INFORMATION FOR SEQ ID NO: 156:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 410 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 96..183  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq IMNLTVMLDTAXG/KX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```

AGAACCACGC CGCTTCCCAG TCTCTGTGCG AGGCGTGAAG CGCGGACCTT TCAACAAGCG    60

```

```

CTTTATTAAT TCTCAGGCTG CGGCGCTGGA AAGCG ATG GAG GTG GCG GCT AAT      113
                Met Glu Val Ala Ala Asn
                -95

TGC TCC CTA CGG GTG AAG AGA CCT CTG TTG GAT CCC CGC TTC GAG GGT      161
Cys Ser Leu Arg Val Lys Arg Pro Leu Leu Asp Pro Arg Phe Glu Gly
-90                -85                -80                -75

TAC AAG BTC TCT CTT GAG GCG CTG CCT TGT TAC CAG CTG GAG CTT GAC      209
Tyr Lys Xaa Ser Leu Glu Pro Leu Pro Cys Tyr Gln Leu Glu Leu Asp
                -70                -65                -60

GCA GCT GTG GCA KAG GTA AAA CTT CGA GAT GAT CAA TAT ACA CTG GAA      257
Ala Ala Val Ala Xaa Val Lys Leu Arg Asp Asp Gln Tyr Thr Leu Glu
                -55                -50                -45

CAC ATG CAT GCT TTT GGA ATG TAT AAT TAC CTG CAC TGT GAT TCA TGG      305
His Met His Ala Phe Gly Met Tyr Asn Tyr Leu His Cys Asp Ser Trp
                -40                -35                -30

TAT CAA GAC AGT GTC TAC TAT ATT GAT ACC CTT GGA AGA ATT ATG AAT      353
Tyr Gln Asp Ser Val Tyr Ile Asp Thr Leu Gly Arg Ile Met Asn
                -25                -20                -15

TTA ACA GTA ATG CTG GAC ACT GCC TTW GGR AAA MCA CGA GAG GTG TTT      401
Leu Thr Val Met Leu Asp Thr Ala Xaa Gly Lys Xaa Arg Glu Val Phe
-10                -5                1                5

CGA CTC CTA      410
Arg Leu Leu

```

## (2) INFORMATION FOR SEQ ID NO: 157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 63..179
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq VLAIGLLHIVLLS/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

```

AGGGACCGA TCCCGGGCCG TTGATCTCG GCGCCACACG AACAGCAGAG AGGGGCATCA      60
GG ATG AAT GTK GGC ACA GCG CAC AGS DAG GTG AAC CCC AAC ACG CGG      107

```

```

Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg
      -35                      -30                      -25

GTK ATG AAC ACC CGT GGC ATC TGG CTC TCC TAC GTG CTG GCC ATC GGT   155
Val Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly
      -20                      -15                      -10

CTC CTC CAC ATC GTG CTG CTG AGC ATC CCG TTT GTK AGT GTC CCT GTC   203
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val
      -5                      1                      5

GTC TGG ACC CTC ACC AAC CTC ATT CAC AAC ATG GGC ATG TAT ATC TTC   251
Val Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe
      10                      15                      20

CTG CAC ACC GTG AAG GGG WCA CCC TTT GAG ACC CCG GAC CAG GGC AAG   299
Leu His Thr Val Lys Gly Xaa Pro Phe Glu Thr Pro Asp Gln Gly Lys
      25                      30                      35                      40

GGG AGG CTG CTW WCC CAC TGG TDA GCA GAT GGA TTA TGG GGT CCA GTT   347
Ala Arg Leu Leu Xaa His Xaa Xaa Ala Asp Gly Leu Trp Gly Pro Val
      45                      50                      55

```

## (2) INFORMATION FOR SEQ ID NO: 158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 8..76
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq SWWTLSSSPSEFM/IS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

```

ATTTATT ATG GAA AAC TTT AAC ATG TAT AAA AAT AAG AGC TGG TGG ACC   49
Met Glu Asn Phe Asn Met Tyr Lys Asn Lys Ser Trp Trp Thr
      -20                      -15                      -10

CTT TTG TCC TCA TCA CCC AGC TTT ATG ATC AGT TTT GTT TCA TCT GTA   97
Leu Leu Ser Ser Ser Pro Ser Phe Met Ile Ser Phe Val Ser Ser Val
      -5                      1                      5

CTA CCA GTG CTA CTT ACC ATC TCT AGG TTC ATT TTG AAG CAA ATC CCA   145
Leu Pro Val Leu Leu Thr Ile Ser Arg Phe Ile Leu Lys Gln Ile Pro
      10                      15                      20

```

GAC CAG  
Asp Gln  
25

151

## (2) INFORMATION FOR SEQ ID NO: 159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 142..258
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq VLAIGLLHIVLLS/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```

AGATTCGGCC GGAGCTGCCA GCGGGGAGGC TGCAGCCGCG GGTGTGTTACA GCTGCTGGAG   60
CAGCAGCGGC CCCCGCTCCC GCGAACCGKT CCCGGGCCGT TGRTCTTCGG CCCACACGA   120
ACAGCAGAGA GGGGCAGCAG G ATG AAT GTG GGS ACA GND CAC AGC GAG GTG   171
          Met Asn Val Gly Thr Xaa His Ser Glu Val
                               -35                -30

AAC CCC AAC ACG CGG GTG ATG AAC AGC CGT GGG ATC TGG CTC TCC TAC   219
Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr
          -25                -20                -15

GTG CTG GCC ATC GGT CTC CTC CAC ATC GTG CTC CTG AGC ATC CCG TTT   267
Val Leu Ala Ile Gly Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe
          -10                -5                1

GTG AGT GTC CCT GTC GTC TGG ACC CTC ACC AAC CTC ATT CAC AAC ATG   315
Val Ser Val Pro Val Val Trp Thr Leu Thr Asn Leu Ile His Asn Met
          5                10                15

GGC ATG TAT ATC TTC CTG TAC ACG GTG AAG GGG ACA   351
Gly Met Tyr Ile Phe Leu Tyr Thr Val Lys Gly Thr
          20                25                30

```

## (2) INFORMATION FOR SEQ ID NO: 160:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 88..129  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq AAASAVSVLLVAA/ER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```

AABGCTTCGT AGTGGAGGAA CGGTTTGGC GTGTGGGACG CAGCTGCCTC TGTACTGGGG    60
AGTCACGGAG TCCCGGGCTC CAGGGAC ATG GCG GCG GCC TCT GCG GTG TCG GTG    114
                               Met Ala Ala Ala Ser Ala Val Ser Val
                               -10

CTG CTG GTG GCG GCG GAG AGG AAC CGG TGG CAT CGT CTC CCG AGC CTG    162
Leu Leu Val Ala Ala Glu Arg Asn Arg Trp His Arg Leu Pro Ser Leu
-5                               1                               5                               10

CTC CTG CCG CCG AGG ACA TGG GTG TGG AGG CAA AGA ACC ATG AAG TAC    210
Leu Leu Pro Pro Arg Thr Trp Val Trp Arg Gln Arg Thr Met Lys Tyr
15                               20                               25

ACA ACA GCC ACA GGA AGA AAC ATC    234
Thr Thr Ala Thr Gly Arg Asn Met
30                               35

```

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 177..308  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq SGSGLSWARLSQS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```

ACTCTTTGCC ACCCTCAGAG GCGAGCTGTG GAAGCCTTGA CTCTTAGGGC CGTTTITAGAA    60
CCGGGGCCTC GGACCGGCGG GGTTCCTGCA CGTGGAAACG GAACATCTGA GATGATCGSM    120
RGGCCCTGTG GAGTGTGGGG AGCCCGGGAG TTCTTTCTTC CCTCGAGGCC CGTGCC ATG    179
                                         Met
GCT TAC TCC AAA GCC AGT GGG TCC CCA GTC CTA AGC CAA GCA GTC CCG    227
Ala Tyr Ser Lys Ala Ser Gly Ser Pro Val Leu Ser Gln Ala Val Pro
      -40                      -35                      -30

GGG GAA AAC GCT TCT CAT CCG CGT GGG AGC GCG GAT CTT GGA AGT GGC    275
Gly Glu Asn Ala Ser His Arg Arg Gly Ser Ala Asp Leu Gly Ser Gly
      -25                      -20                      -15

TCT GGG CIT TCT TGG GCG AGG CTC TCA CAG AGT AGA TCG GAA ATC CAT    323
Ser Gly Leu Ser Trp Ala Arg Leu Ser Gln Ser Arg Ser Glu Ile His
      -10                      -5                      1                      5

TCT GCT GGC CCG CCC CAC CTC GGA GGA CCG ACT AAC GGA CCT GAG TTC    371
Ser Ala Gly Pro Pro His Leu Gly Gly Arg Thr Asn Gly Pro Glu Phe
              10              15              20

CCG GCC CTA TCT TAC TCT TCT CAG CTT CTC AGC TTG GCT CAG CTC AGA    419
Pro Ala Leu Ser Tyr Ser Ser Gln Leu Leu Ser Leu Ala Gln Leu Arg
              25              30              35

GGA AGA GGA ATC ACT GAA GTC TCA GAG AAG TCT CCA CTC ATC    461
Gly Arg Gly Ile Thr Glu Val Ser Glu Lys Ser Pro Leu Ile
              40              45              50

```

## (2) INFORMATION FOR SEQ ID NO: 162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 175..285
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq RPVLLHLHQTAHA/DE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```

AGGCTCCGCG CTCTGGAGGC TCAGGCGCCG CGTGGGGCCC GCACCTCTGG GCAGCAGCGG    60

```



CAGCCGAGAC TCACGGTCAA GCTAAGSCGA AGASTGGGCTG GCTGAAGCCA TACTATTTTA 120  
 TAGAATTAAT GGRAARCMHG AAAAGMCATC ACAAAACCAAG AAGAACTTTG GAAA ATG 177  
 Met  
 AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG 225  
 Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr  
 -35 -30 -25  
 GGA GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA 273  
 Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln  
 -20 -15 -10 -5  
 ACA GCC CAT GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA 321  
 Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr  
 1 5 10  
 CAG GAA CTC TTT CCA CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT 369  
 Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile  
 15 20 25  
 ATA GCA TCT CTG ACT TTT CTT TAC ACT CTT CTG AGC GAA GTA ATT CAC 417  
 Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His  
 30 35 40  
 CCT TTA GCA ACT TCC CAT CAA CAA TAT TTT TAT AAA ATT CAA 459  
 Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Gln  
 45 50 55

## (2) INFORMATION FOR SEQ ID NO: 163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 25..81
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq IPCAHMLVCPTIG/DI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

AATTTGTAAG AATATTATAT ATAG ATG ATC ATC TGT TAT GAT ATT CCT TGT 51  
 Met Ile Ile Cys Tyr Asp Ile Pro Cys  
 -15  
 GCA CAT ATG TTG GTT TGT CCT ACT ATT CGT GAT ATT AAG TTT GAT CAC 99  
 Ala His Met Leu Val Cys Pro Thr Ile Gly Asp Ile Lys Phe Asp His

-10	-5	1	5	
TTG ATG AAG TGG TAT CCA TCA GAT TTC TCT ACT GAA AGG CTG				141
Leu Met Lys Trp Tyr Pro Ser Asp Phe Ser Thr Glu Arg Leu				
10	15	20		

## (2) INFORMATION FOR SEQ ID NO: 164:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 184..240
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq STLASVPPAATFG/AD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

AACCAGGCTC TATTTAGAGC CGGGTAGGGG AGCGCAGGNC CAGATACCTC ASCGCTACCT	60
GGCGGAACTG GATTTCTCTC CCGCCTGCCG GCCTGCCCTGC CACAGCCGGA CTCCGCCACT	120
CCGGTAGCCC CATGGCTGGM AACCTGTGAG ATTAGCAATA TTTTAGCAA CTACTTCAGT	180
GCG ATG TAC AGC TCG GAG GAC TCC ACC CTG GCC TCT GTT CCC CCT GCT	228
Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala	
-15 -10 -5	
GCC ACC TTT GGG GCC GAT GAC TTG GTA CTG ACC CTG AGC AAC CCC CAG	276
Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln	
1 5 10	
ATG TCA TTG GAG GGT ACA GAG AAG GCC AGC TGG TTG GGG GAA CAG CCC	324
Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro	
15 20 25	
CAG TTC TGG TCG AAG ACG CAG GTT CTG GAC TGG ATC AGC TAC CAA GTG	372
Gln Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val	
30 35 40	
GAG AAG AAC AAG TAC GAC GCG	393
Glu Lys Asn Lys Tyr Asp Ala	
45 50	

## (2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 263 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 54..248  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq QLEGLNWLRFSSWA/QG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```

ACCCTGAATA CGAAGAACAT AAGCAAAGCT ACTGGAGACA CCSAGAACTA ATT ATG      56
                                     Met
                                     -65

GGG GAA GAC CCT KCC CAG CCC CGC AAG TAT AAG AAG WWG AAG AWG GAG      104
Gly Glu Asp Pro Xaa Gln Pro Arg Lys Tyr Lys Lys Xaa Lys Xaa Glu
      -60                      -55                      -50

CTA CAG GGT GAT KGG CCT CCC AGT TCT CCC ACT AAT GAT CCT ACC GTG      152
Leu Gln Gly Asp Xaa Pro Pro Ser Pro Thr Asn Asp Pro Thr Val
      -45                      -40                      -35

AAA TAT GAG ACT CAG CCA CGG TTT ATC ACA GCC ACT GGA GGC ACC CTG      200
Lys Tyr Glu Thr Gln Pro Arg Phe Ile Thr Ala Thr Gly Gly Thr Leu
      -30                      -25                      -20

CAC ATG TAT CAG TTG GAA GGG CTG AAC TGG CTA CGC TTC TCC TGG GCC      248
His Met Tyr Gln Leu Glu Gly Leu Asn Trp Leu Arg Phe Ser Trp Ala
      -15                      -10                      -5

CAG GGC ACT KWC GGG
Gln Gly Thr Xaa Gly
      1                      5
                                     263

```

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 372 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 148..273  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq LLGCLQCCWLQSG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```

ACCAATTTTG TAGTTATCTG ATCTGAAGGA AGATGTGTGT GGAGGTGTTT AGTGATGTTT   60
TCCSATGACG GTGATTCGCC CTAAATCTAC GTATTAAATA CAATGGAACA GSATCCACAG   120
TTCACCCCTA ATAATATAGT TTACTGA ATG TTT TAT GTA GCT ATG ACC AAA ACT   174
                               Met Phe Tyr Val Ala Met Thr Lys Thr
                               -40                               -35
CAC AAA AGG ATC AGA AGC CTC TGT AAC ATC CAC CAT GGT TTG TTC CAG   222
His Lys Arg Ile Arg Ser Leu Cys Asn Ile His His Gly Leu Phe Gln
                               -30                               -25                               -20
TTT ACT CAG CAG CTC CTG GGC TGT CTT CAG TGC TGT TGG CTG CAA TCA   270
Phe Thr Gln Gln Leu Leu Gly Cys Leu Gln Cys Cys Trp Leu Gln Ser
                               -15                               -10                               -5
GGC AGA GCC CCA GCT ACC TAT TAC CTT GTG GAG AGT ATT GAA AAG TCA   318
Gly Arg Ala Pro Ala Thr Tyr Tyr Leu Val Glu Ser Ile Glu Lys Ser
                               1                               5                               10                               15
GCA CAT GGC TCT GTA TTA NGT ACT TAT GAT CAA ACT CAG ACT CGC ATA   366
Ala His Gly Ser Val Leu Xaa Thr Tyr Asp Gln Thr Gln Thr Arg Ile
                               20                               25                               30
GGC AGG   372
Gly Arg
  
```

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 158..337  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq XTCASXNPSQCLA/AF

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```

ACAGAATCTT TAGGTGGGCC TSTTGGT3AG GTCACTTTTC CCTAATCGTA TATTCCAGTT      60
CCTGTAGATC CTATTCCAGT TCCCAGGACA TATTCCAAGG TCGACCTCCA GCCAACTTTG    120
AAGCCCTGAA GTTGTGTGCT GATGTGTTTC TAACAAC ATG GTC TCA CCC AAA GAT      175
                               Met Val Ser Pro Lys Asp
                               -60                               -55
CTT CCT CTT GTG CTT TTG CAG GAC ATT AAA GTT CCC AGC TCC ATG ACT      223
Leu Pro Leu Val Leu Leu Gln Asp Ile Lys Val Pro Ser Ser Met Thr
                               -50                               -45                               -40
GGA TCA CAT GCT GGA AAC CCT CAT ATA GAA AGG AAT GAT CTC CCC AGA      271
Gly Ser His Ala Gly Asn Pro His Ile Glu Arg Asn Asp Leu Pro Arg
                               -35                               -30                               -25
CAT GGT TCT CCT CAA TTT TTT ACA GGH HYG ACT TGT GCT TCT RCA AAC      319
His Gly Ser Pro Gln Phe Phe Thr Gly Xaa Thr Cys Ala Ser Xaa Asn
                               -20                               -15                               -10
CCA TCT CAG TGT CTG GCA GCA TTT                                      343
Pro Ser Gln Cys Leu Ala Ala Phe
                               -5                               1

```

## (2) INFORMATION FOR SEQ ID NO: 168:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..45
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq FXSLFCLYFSCFL/HI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```

ATG GAA TTT KTT TCT CTT TTC TGT CTC TAC TTC AGC TGT TTC CTA CAT      48
Met Glu Phe Xaa Ser Leu Phe Cys Leu Tyr Phe Ser Cys Phe Leu His
-15                               -10                               -5                               1
ATT ATA TAT TTT KKC AGC TGT TTC CTA TAC                                73
Ile Ile Tyr Phe Xaa Ser Cys Phe Leu Tyr
5                               10

```

## (2) INFORMATION FOR SEQ ID NO: 169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 10..144
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq ALLELIDSPECLS/KC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```

ACTGGGAAG ATG GCG CTG CAC TTC CAG AGT TTG GCT GAA TTG GAA RTG TTA      51
  Met Ala Leu His Phe Gln Ser Leu Ala Glu Leu Glu Xaa Leu
    -45                -40                -35

TGT ACT CAT CTC TAC ATA GGG ACT GAT CTT ACA CAA AGA ATA GAG GCT      99
  Cys Thr His Leu Tyr Ile Gly Thr Asp Leu Thr Gln Arg Ile Glu Ala
    -30                -25                -20

GAG AAA GCA CTC TTG GAA CTT ATT GAC AGT CCA GAA TGT CTC AGC AAG     147
  Glu Lys Ala Leu Leu Glu Leu Ile Asp Ser Pro Glu Cys Leu Ser Lys
    -15                -10                -5                1

TGT CAA CTT TTA TTA GAA CAA GGA ACA ACA TCC TAT GCT CAG CTC CTT     195
  Cys Gln Leu Leu Leu Glu Gln Gly Thr Thr Ser Tyr Ala Gln Leu Leu
    -                5                10                15

GCA GCA ACC GKV                                                    207
  Ala Ala Thr Xaa
    20

```

## (2) INFORMATION FOR SEQ ID NO: 170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 299..379
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq LTLLLITPSPSPL/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```

ACCTTGGGCT CCAAATTCTA GCTCATAAAG ATGCAAGTKT TGCAATTTCG TATAAATGCT   60
TAAGAAAAGA GCAAGCTGTC CAGAGAGTGA GAAGTTTGAA AAGAGAGGCT CATAAGAGAG   120
AAATGATGTC CATTTGAGCC CCACCACGGA GGTTATGTGG TCCCAAAGG AATGATGGCC   180
AAGCAATTAA TTTTCCTCC TAGTCTTAG CTGCTTCTG CATTGATTGG CTTIACACAA   240
CTGGCATTTA GTCTGCATTA CACAAATAGA CACTAATTTA TTTGGAACAA GCAGCAAA   298
ATG AGA ACT TTA TTT GGT GCA GTC AGG GCT CCA TTT AGT TCC CTC ACT   346
Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
      -25                -20                -15

CTG CTT CTA ATC ACC CCT TCT CCC AGC CCT CTT CTA TTT GAT AGA GGT   394
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
      -10                -5                1                5

CTG TCC CTC AGA TCA GCA ATG TCG   418
Leu Ser Leu Arg Ser Ala Met Ser
              10

```

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 107..229
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq AVSSLIAVGTSHG/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```

ACACTCCTAT GATACTTCAT CTGTGGCAAG CTCAGATAGT GSTGACAGGA CCACTTAAA   60

```

AAGGAAGAAG	AAATTACCTG	ATTCTTTTTC	ACTTCATGGA	TCAGTT	ATG	GCG	CAT		115							
							Met Arg His									
							-40									
TCA	CTT	TTG	AAG	GGA	ATT	TCT	GCC	CAG	ATA	GTG	TCT	GCA	GCT	GAC	AAA	163
Ser	Leu	Leu	Lys	Gly	Ile	Ser	Ala	Gln	Ile	Val	Ser	Ala	Ala	Asp	Lys	
			-35					-30						-25		
GTA	GAT	GCT	GGC	TTG	CCT	ACA	GCA	ATT	GCA	GTA	TCC	AGT	CTG	ATA	GCA	211
Val	Asp	Ala	Gly	Leu	Pro	Thr	Ala	Ile	Ala	Val	Ser	Ser	Leu	Ile	Ala	
			-20					-15					-10			
GTG	GGT	ACA	TCT	CAT	GGA	TTG	GCT	GGG								238
Val	Gly	Thr	Ser	His	Gly	Leu	Ala	Gly								
			-5					1								

(2) INFORMATION FOR SEQ ID NO: 172:

## (2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(v1) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 120..164  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LSCFIFFYISSLC/CF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

TGTGAAGATG ACAGAGATCT AACTTCTGAG AGCAGAGGTG TCAAGTGACG GTCCCCCTTGG	60
AGGAATGGTC TTTGCATCTG ACTACTTCCT TCTGCAACTG TGTTCTTCCA TTAGCTTCC	119
ATG ACA CTC TCC TGC TTT ATT TTT TTC TAC ATC TCT AGC CTT TGC TGT	167
Met Thr Leu Ser Cys Phe Ile Phe Phe Tyr Ile Ser Ser Leu Cys Cys	
-15                      -10                                  -5    1	
TTC CTC TCC TAC CCC ACC AGG	188
Phe Leu Ser Tyr Pro Thr Arg	
5	

## (2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs



(B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 28..72  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
 seq LCFLLPHRLQEA/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```

ATAGATCAGT GACGTCTTTT TCTTCAG ATG ATC CTA TGT TTC CTT CTT CCT CAT   54
                        Met Ile Leu Cys Phe Leu Leu Pro His
                        -15                               -10

CAT CGT CTT CAG GAA GCC AGA CAG ATT CAA GTA TTG AAG ATG CTG CCA   102
His Arg Leu Gln Glu Ala Arg Gln Ile Gln Val Leu Lys Met Leu Pro
   -5                               1                               5                               10

AGG GAA AAA TTA AGR AGA AGR AGA AGA GAG AAA ACA AAT AAA TGG GAA   150
Arg Glu Lys Leu Arg Arg Arg Arg Glu Lys Thr Asn Lys Trp Glu
           15                               20                               25

AAA AGA AAG GGC AGC GGG                                           168
Lys Arg Lys Gly Ser Gly
           30
  
```

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 64..105  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
 seq FSLFALNMPLGFC/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

```

TATATTTTAA CCATCTTTTA CTATTTTATAG AAGGAACTA GCTTAGTAG TGGGTGGCC 60
TGT ATG TTT TCT CTT TTT GCT CTT AAT ATG CCA TTG GGT TTT TGT GTG 108
Met Phe Ser Leu Phe Ala Leu Asn Met Pro Leu Gly Phe Cys Val
      -10      -5      1

TAT GTG ATT TTC AAA ATT CAT GAC TGG 135
Tyr Val Ile Phe Lys Ile His Asp Trp
      5      10

```

## (2) INFORMATION FOR SEQ ID NO: 175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 163..255
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq SVWGVLPSPACSA/DL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```

ATTTGATTTT AGTCAGGGTG TAAGAATATG TATTATTGTT CCCAAAAAAA TCTGTGTAAA 60
AACTTCATAG TGTGAAACAG TGGCAACTGS KTGATTAAAA CATCATTTAG AAAAGACACT 120
CTTCCCTGTT TTGAAATTGA CTCCTCAAAA GGACAGCTGA AC ATG GCC TCT TCT 174
Met Ala Ser Ser
      -30

CCA GGT GTC GCC ATG CAC TCC CTC TGG GCC ACC ATA CAC ACT TCT GTG 222
Pro Gly Val Ala Met His Ser Leu Trp Ala Thr Ile His Thr Ser Val
      -25      -20      -15

TGG GGC GTG CTC CCA CCT CCA GCC TGC TCA GCT GAT CTT TTG TTC AGC 270
Trp Gly Val Leu Pro Pro Pro Ala Cys Ser Ala Asp Leu Leu Phe Ser
      -10      -5      1      5

AAT GCC TGT CTA CTT CCC CAT GAG ATC CAC CTG 303
Asn Ala Cys Leu Leu Pro His Glu Ile His Leu
      10      15

```

## (2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 317 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 60..194  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
 seq LPRLLSLSQHSSES/WI
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```

AGAGTTTCCG GTCTGGGCTT TGGCGGGTCT GGTTTGAAGC TCTCCTGTTT GACGAAAGT      59

ATG TCT CAG GAA GGT GCG GTC CCA GCT AGC GCG GTT CCC CTG GAA GAA      107
Met Ser Gln Glu Gly Ala Val Pro Ala Ser Ala Val Pro Leu Glu Glu
-45                -40                -35                -30

TTA AGT AGC TGG CCA GAG GAG CTA TGC CGC CGG GAA CTG CCG TCC GTC      155
Leu Ser Ser Trp Pro Glu Glu Leu Cys Arg Arg Glu Leu Pro Ser Val
                -25                -20                -15

CTG CCC CGA CTC CTC TCA TTG TCT CAA CAT TCT GAA AGT TGG ATT GAG      203
Leu Pro Arg Leu Leu Ser Leu Ser Gln His Ser Glu Ser Trp Ile Glu
                -10                -5                1

CAT ATT CAA ATT TTG AAA ATT ATT GTA GAA ATG TTT TTA CCT CAT ATG      251
His Ile Gln Ile Leu Lys Ile Ile Val Glu Met Phe Leu Pro His Met
  5                10                15

AAC CAC CTG ACA TTG GAA CAG ACT TTC TTT TCA CAA GTG TTA CCA AAG      299
Asn His Leu Thr Leu Glu Gln Thr Phe Phe Ser Gln Val Leu Pro Lys
  20                25                30                35

ACT GTG AAA TTA TTC GAT
Thr Val Lys Leu Phe Asp
                40

```

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 254..361  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq AAVVFAVVLSIHA/TV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```

AGTAACTGTG AGGAAGGCTG CAGAGTGGCG ACGTCTACGC CGTAGGTTGS AGGCTGTGGG    60
GGGTGGCCCG GGGCCAGGTC CCAGGCCGCA GAAGTGACCT GCGGTGGAST TCCCTCCTCG    120
CTGCTGGAGA ACGGAAGGGA ARAAGGTTSC TGGCCGGGTG AAAGTGCCTC CCTCTGCTTG    180
ACGGGGCTGA GGGGCCCCGAA GTCTAGGGCG TCCGTAGTCG CCCCGGCCTC CGTGAAGCCC    240
CAGGTCTAGA GAT ATG ACC CGA GAG TGC CCA TCT CCG GCC CCG GGG CCT    289
      Met Thr Arg Glu Cys Pro Ser Pro Ala Pro Gly Pro
      -35                -30                -25

GGG GCT CCG CTG AGT GGA TCG GTG CTG GCA GAG GCG GCA GTA GTG TTT    337
Gly Ala Pro Leu Ser Gly Ser Val Leu Ala Glu Ala Ala Val Val Phe
      -20                -15                -10

GCA GTG GTG CTG AGC ATC CAC GCA ACC GTA TGG    370
Ala Val Val Leu Ser Ile His Ala Thr Val Trp
      -5                1

```

## (2) INFORMATION FOR SEQ ID NO: 178:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 369..470  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 2..103  
id AA059664  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 216..263

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 14.8  
 seq LLWWALLLLGLAQA/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```

AAGTGGATGG TTCCAGGCAC CCTGTCTGGG GCAGGGAGGG CACAGGCTG CACATCGAAG 10
GTGGGGTGGC ACCAGGCTCC CCCTGCCCCC AGCATCCAAG TCCTCCCTTG GGC3CCCGTG 120
GCCCTGGCAG ACTCTCAGGG STAAGGTCCT CTGTIGCTTT TTGGTTCCAC CTTAGAAGAG 180
GCTCGCTTGA CTAAGASTAG CTTGAAGGAG GCACC ATG CAG GAG CTG CAT CTG 233
                               Met Gln Glu Leu His Leu
                               -15

CTC TGG TGG GCG CTT CTC CTG GCC CTG GCT CAG GCC TGC CCT GAG CCC 281
Leu Trp Trp Ala Leu Leu Leu Gly Leu Ala Gln Ala Cys Pro Glu Pro
-10 -5 1

TGC GAC TGT GGG GAA AAG TAT GGC TTC CAG ATC GCC GAC TGT GCC TAC 329
Cys Asp Cys Gly Glu Lys Tyr Gly Phe Gln Ile Ala Asp Cys Ala Tyr
5 10 15 20

CGC GAC CTA GAA TCC GTG CCG CCT GGC TTC CCG GCC AAT GTG ACT ACA 377
Arg Asp Leu Glu Ser Val Pro Pro Gly Phe Pro Ala Asn Val Thr Thr
25 30 35

CTG AGC CTG TCA GCC AAC CGG CTG CCA GGC TTG CCG GAR GGT GCC TTC 425
Leu Ser Leu Ser Ala Asn Arg Leu Pro Gly Leu Pro Glu Gly Ala Phe
40 45 50

AGG GAG GTG CCC CTG CTG CAG TCG CTG TGG CTG GCA CAC AAT GAG 470
Arg Glu Val Pro Leu Leu Gln Ser Leu Trp Leu Ala His Asn Glu
55 60 65

```

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 69..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
 region 1..260  
 id H96534  
 est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 14..67
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.6  
seq LLLLALCATGAQG/LY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

CTCTCTGCGG GCG ATG GGG CGG CAG GCC CTG CTG CTT CTC GCG CTG TGC      49
      Met Gly Arg Gln Ala Leu Leu Leu Leu Ala Leu Cys
                -15                      -10

GCC ACA GGC GGC CAG GGG CTC TAC TTC CAC ATC GGC GAG ACC GAG AAG      97
Ala Thr Gly Ala Gln Gly Leu Tyr Phe His Ile Gly Glu Thr Glu Lys
      -5                      1                      5                      10

CGC TGT TTC ATC GAG GAA ATC CCC GAC GAG ACC ATG GTC ATC GGC AAC      145
Arg Cys Phe Ile Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly Asn
                15                      20                      25

TAT CGT ACC CAG ATG TGG GAT AAG CAG AAG GAG GTC TTC CTG CCC TCG      193
Tyr Arg Thr Gln Met Trp Asp Lys Gln Lys Glu Val Phe Leu Pro Ser
                30                      35                      40

ACC CCT GGC CTG GGC ATG CAC GTG GAA GTG AAG GAC CCC GAC GGC AAG      241
Thr Pro Gly Leu Gly Met His Val Glu Val Lys Asp Pro Asp Gly Lys
                45                      50                      55

GTG GTG CTG TCC CGG CAG TAC GGC TCG GAG GGC CGC TTC ACG TTC ACC      289
Val Val Leu Ser Arg Gln Tyr Gly Ser Glu Gly Arg Phe Thr Phe Thr
                60                      65                      70

TCC CAC ABN KSG GGT GAC CAT CAA ATC TGT CTG CAC TGC GGG      331
Ser His Xaa Xaa Gly Asp His Gln Ile Cys Leu His Cys Gly
      75                      80                      85

```

## (2) INFORMATION FOR SEQ ID NO: 180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..40

id AA134726  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 157..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 66..104  
id AA134726  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..156  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 34..66  
id AA134726  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 107..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..89  
id R17226  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 76..138  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 12.7  
seq ILFLLSWGPLQG/QQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

```

AAGCTAACCC TCGGGCTTGA GGGGAAGAGG CTGACTGTAC GTTCCTTCTA CTCTGGCACC    60
ACTCTCCAGG CTGCC ATG GGG CCC AGC ACC CCT CTC CTC ATC TTG TTC CTT    111
      Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu
      -20                      -15                      -10

TTG TCA TGG TCG GGA CCC CTC CAA GGA CAG CAG CAC CAC CTT GTG GAG    159
Leu Ser Trp Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu
      -5                      1                      5

TAC ATG GAA CGC CGA CTA GCT GCT TTA GAG GAA CGG    195
Tyr Met Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg
      10                      15

```

## (2) INFORMATION FOR SEQ ID NO: 181:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 base pairs  
(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 313..349  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 7..43  
id T67245  
est

(ix) FEATURE:

(A) NAME/KEY: sig peptide  
(B) LOCATION: 119..199  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.8  
seq LLLLCPLSRGCCP/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```

ACGTTACCTT TGGGTGGTGG TTTTCATGCC TGTGCCGCCT GCTTCTGGGC CAGTGATCCA   60
GGTGTCTGGT GACCACCCGG GCACAGCTGC TTGGCTGCTG TGGGCACCTC AGCTTCCC   118
ATG TCC TGT AGG GAA CTC ACC CAC CGG CCT TGC TCT CCA CAC CTC TTA   166
Met Ser Cys Arg Glu Leu Thr His Arg Pro Cys Ser Pro His Leu Leu
      -25                      -20                      -15
CTC CTG TGT CCC CTT TCT CGG GGA TGC TGC CCC CTC CTG CTG TCC KGT   214
Leu Leu Cys Pro Leu Ser Arg Gly Cys Cys Pro Leu Leu Leu Ser Xaa
      -10                      -5                      1                      5
CCY CTG TWA GGG GTG AAT CTT GAA TCC ATC TTA TCT CTT ACT CTC CCT   262
Pro Leu Xaa Gly Val Asn Leu Glu Ser Ile Leu Ser Leu Thr Leu Pro
              10                      15                      20
CCC TCT CCC AGC TCA GTC GGG CTC TCA CCC TCT GTG ACC CAS CTC ACA   310
Pro Ser Pro Ser Ser Val Gly Leu Ser Pro Ser Val Thr Xaa Leu Thr
              25                      30                      35
ACT TCA CCT GTT TCA TTG CAC TTT GCA TCC GMC CTC GCC GGG   352
Thr Ser Pro Val Ser Leu His Phe Ala Ser Xaa Leu Ala Gly
              40                      45                      50

```

(2) INFORMATION FOR SEQ ID NO: 182:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 113..306

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 71..264  
id H83784  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 42..111

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..70  
id H83784  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 378..414

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 346..382  
id H83784  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 305..340

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 264..299  
id H83784  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 250..350

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 2..102  
id W32197  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 392..449

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 142..199  
id W32197  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 349..390  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 100..141  
                           id W32197  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 397..449  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..53  
                           id W37255  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 85..150  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.5  
                           seq AALLLGLMMVVVG/DE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

```

AACTTGTGTC CGGGTGCWRG ACTGGATTAG CTGCGGASCC TGAAGCTGC CTGTCCTTCT      60
CCCTGTGCTT AACCAGAGGT GCCC ATG GGT TGG ACA ATG AGG CTG GTC ACA      111
               Met Gly Trp Thr Met Arg Leu Val Thr
               -20                      -15

GCA GCA CTG TTA CTG GGT CTC ATG ATG GTG GTC ACT GGA GAC GAG GAT      159
Ala Ala Leu Leu Leu Gly Leu Met Met Val Val Thr Gly Asp Glu Asp
          -10                      -5                      1

GAG AAC AGC CCG TGT GCC CAT GAG GCC CTC TTG GAC GAG GAC ACC CTC      207
Glu Asn Ser Pro Cys Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu
          5                      10                      15

TTT TGC CAG GGC CTT GAA GTT TTC TAC CCA GAG TTG GGG AAC ATT GGC      255
Phe Cys Gln Gly Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly
          20                      25                      30                      35

TGC AAG GTT GTT CCT GAT TGT DAC AAC TAC AGA CAG AAG ATC ACC TCC      303
Cys Lys Val Val Pro Asp Cys Xaa Asn Tyr Arg Gln Lys Ile Thr Ser
               40                      45                      50

TGG ATG GAG CCG ATA GTC AAG TTC CCG GGG GCC GTG GAC GGC GCA ACC      351
Trp Met Glu Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr
               55                      60                      65

TAT ATC CTG GTG ATG GTG GAT CCA GAT GCC CCT AGC AGA GCA GAA CCC      399
Tyr Ile Leu Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro
          70                      75                      80

AGA CAG AGA TTC TGG AGA CAT TGG CTG GTA ACA GAT ATC AAG GGC GCC      447
Arg Gln Arg Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala
          85                      90                      95

```

## (2) INFORMATION FOR SEQ ID NO: 183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..182
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 6..63  
id R18560  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..213
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 58..95  
id R18560  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..182
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..38  
id R13864  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..213
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 33..70  
id R13864  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..213
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 2..39  
id HSC01E071  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 113..190
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq VHLLSLCSGKVYA/RM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```

ACTGGGAGCC GCCTCCGTCG CCGCCGTCAG AGCCGCCCTA TCAGAGTTCC TACCANTTTG   60
TGSTCCAGC AGCTTCTGTT CCAGATTATC TTAACAAGAA AACCAACTGG AAAAAAAAAA   118
ATG AAA TTC CTT ATC TTC GCA TTT TTC GGT GGT GTT CAC CTT TTA TCC   168
Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
      -20                      -15                      -10
CTG TGC TCT GGG AAA GTA TAT GCA AGA ATG GCA TCT CTA AGA GGA CTC   214
Leu Cys Ser Gly Lys Val Tyr Ala Arg Met Ala Ser Leu Arg Gly Leu
      -5                      1                      5
GGG
Gly
217

```

## (2) INFORMATION FOR SEQ ID NO: 184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 139..361
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 92..314  
id AA100852  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..434
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 314..388  
id AA100852  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 139..434  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 100..395  
id AA224847  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 139..361  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 92..314  
id AA161042  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 368..434  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 323..389  
id AA161042  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 139..365  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 87..313  
id H64488  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 52..144  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 1..93  
id H64488  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 171..396  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 129..354  
id AA088770  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 167..253  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.1  
seq LIFLCCGALLAVG/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```

AAAAAGCGCC TACCCTGCCT GCASGTGAGC AGTGGTGTGT GAGAGCCAGG CGTCCCTCTG   60
CCTGCCCCACT CAGTGGCAAC ACCCGGGAGC TGTTTTGTCC TTTGTGGAGC CTCAGCAGTT  120
CCCTCTTTCA GAACTYRVYK GCCAAGAGCC CTGAACAGGA GCCACC ATG CAG TGC   175
                               Met Gln Cys
TTC AGC TTC ATT AAG ACC ATG ATG ATC CTC TTC AAT TTG CTC ATC TTT   223
Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe
-25                               -20                               -15
CTG TGT GGT GCA GCC CTG TTG GCA GTG GGC ATC TGG GTG TCA ATC GAT   271
Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val Ser Ile Asp
-10                               -5                               1                               5
GGG GCA TCC TTT CTG AAG ATC TTC GGG GCA CTG TCG TCC AGT GCC ATG   319
Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser Ser Ala Met
                               10                               15                               20
CAG TTT GTC AAC GTG GGC TAC TTC CTC ATC GCA GCC GGC GTT GTG GTC   367
Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly Val Val Val
                               25                               30                               35
TTT GCT CTT GGT TTC CTG GGC TGC TAT GGT GCT AAG ACT GAG AGC AAG   415
Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr Glu Ser Lys
                               40                               45                               50
TGT GCC CTC GTG ACG TTC                                           433
Cys Ala Leu Val Thr Phe
55                               60

```

## (2) INFORMATION FOR SEQ ID NO: 185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 1..115  
id R58075  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 220..303

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.6

seq IVSLLGFVATVTL/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

```

AAGATAAGCG GGTGCAGCGG GGCAGAACAT AGGTTGCCTT AGAGAGGTTT CCGGAGTCC   60
CGACGGCGGC TCAAGTCAGA GTTGCTGGGT TTGCTCAGA TTGGTGTGGG AAGAGCCTGC  120
CTGTGGGGAG CGGCCACTCC ATACTGCTGA GGGCTCAGGA CTGCTGCTCA GCTTGCCCGT  180
TACCTGAAGA GGCGGCGGAS GGGCCCCTGA GGGGTACCC ATG TGG GCC TTC TCG   234
                               Met Trp Ala Phe Ser
                               -25

GAA TTG CCC ATG CCG CTG CTG ATC AAT TTG ATC GTC TCG CTG CTG GGA   282
Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile Val Ser Leu Leu Gly
          -20                      -15                      -10

TTT GTG GCC ACA GTC ACC CTC ATC CCG GCC TTC CGG GGC CAC TTC ATT   330
Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe Arg Gly His Phe Ile
          -5                      1                      5

GCT GCG CGC CTC TGT GGT CAG GAC CTC AAC AAA ACC AGC CAG           372
Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys Thr Ser Gln
  10                      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 112..403

(C) IDENTIFICATION METHOD: blastn

```

(D) OTHER INFORMATION: identity 97
                        region 33..324
                        id H97426
                        est

```

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 59..295

(C) IDENTIFICATION METHOD: blastn

```

(D) OTHER INFORMATION: identity 98
                        region 2..239
                        id W44834

```

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 106..156  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 4..54  
 id R57989  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 161..190  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 62..91  
 id R57989  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 148..204  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.3  
 seq VLMRLVASAYSIA/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```

AGCTGAGGTA GGGATGCSAT CCTTCTCAAA AGACTTATTG ACAGTGCCAA AGCTSGGTAC   60
TGGACACAAC GAGGCACCTG GGTCTACGAT AACGCGCTTK TGCTCCTCCT GAAGTGTCTT  120
TGGTCCAACG TTGTTCCAGA GTGTACC ATG GCT TCC AGT AAC ACT GTG TTG ATG   174
                               Met Ala Ser Ser Asn Thr Val Leu Met
                               -15

CGG TTG GTA GCC TCC GCA TAT TCT ATT GCT CAA AAG GCA GGD ATG ATA   222
Arg Leu Val Ala Ser Ala Tyr Ser Ile Ala Gln Lys Ala Gly Met Ile
-10                               -5                               1                               5

GTC AGA CGT GTT ATT GCT GAA GGA GAC CTG GGT ATT GTG GAG ADG ACC   270
Val Arg Arg Val Ile Ala Glu Gly Asp Leu Gly Ile Val Glu Xaa Thr
    10                               15                               20

TGT GCA ACA GAC CTG CAG ACC AAA GCT GAC CGA TTG GCA CAG ATG AGN   318
Cys Ala Thr Asp Leu Gln Thr Lys Ala Asp Arg Leu Ala Gln Met Xaa
    25                               30                               35

ATA TGT TCT TCA TTG GCC CGG AAA TTC CCC AAA CTC ACA ATT ATA GGG   366
Ile Cys Ser Ser Leu Ala Arg Lys Phe Pro Lys Leu Thr Ile Ile Gly
    40                               45                               50

GAA GAG GAT CTG CCT TCT RMG GAA GTG GAT CAA GAG                   402
Glu Glu Asp Leu Pro Ser Xaa Glu Val Asp Gln Glu
    55                               60                               65

```

## (12) INFORMATION FOR SEQ ID NO: 187:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 317 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 111..318  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 6..213  
                            id R18560  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 131..318  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 1..188  
                            id R13864  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 162..318  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 1..157  
                            id HSC01E07!  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 207..318  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 1..112  
                            id AA016124  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: 105..176  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 5.9  
                            seq VHLLSLCSGKAIC/KN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18/:

AAGTAAGGCT AGGYCGCGAG CTTAGTCCTG GGAGCCGCGCT CGTCGCGCGC CGTCAGAGCC 60

```

GCCCTATCAG ATTATCTTAA CAAGAAAACC AACTGGAAAA AAAA ATG AAA TTC CTT 116
                                   Met Lys Phe Leu

ATC TTC GCA TTT TTC GGT GGT GTT CAC CTT TTA TCC CTG TGC TCT GGG 164
Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser Leu Cys Ser Gly
-20                               -15                -10                -5

AAA GCT ATA TGC AAG AAT GGC ATC TCT AAG AGG ACT TTT GAA GAA ATA 212
Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr Phe Glu Glu Ile
                               1                   5                   10

AAA GAA GAA ATA GCC AGC TGT GGA GAT GTT GCT AAA GCA ATC ATC AAC 260
Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys Ala Ile Ile Asn
                               15                   20                   25

CTA GCT GTT TAT GGT AAA GCC CAG AAC AGA TCC TAT GGC CGA TTG GCA 308
Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr Xaa Arg Leu Ala
                               30                   35                   40

CTT CTG GTT 317
Leu Leu Val
43

```

## (2) INFORMATION FOR SEQ ID NO: 188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 59..300  
id H29377  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 454..499
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 356..401  
id H29377  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..179
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 36..79  
id H29377  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 397..436  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 297..336  
id H29377  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..295  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 293..453  
id N28905  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..127  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 4..86  
id N28905  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 334..388  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 489..543  
id N28905  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..395  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 81..341  
id H11885  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 160..334  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 105..329  
id H15231  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 136..181  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 82..127  
 id H15231  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 146..298  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.9  
 seq ALXVLP LLGLHEA/AS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```

AACTCCGGG TTCGGCAATA ACCTGGAGCC GCGCGCGTAG GTTGGCTCTT TAGGGCTTCA    60
CCCCGAAGCT CCACCTTCGC TCCCTCTTT CTGAAACAC CGCTTTGATC TCGGCGGTGC    120
GGGACAGACG CTAGTGTGAG CCNMC ATG GCA GAT ACG ACC CCG AAC GGC CCC    172
                        Met Ala Asp Thr Thr Pro Asn Gly Pro
                        -50                                -45
CAA GGG GCG GGC GCT GTG CAA TTC ATG ATG ACC AAT AAA CTG GAC ACG    220
Gln Gly Ala Gly Ala Val Gln Phe Met Met Thr Asn Lys Leu Asp Thr
      -40                                -35                                -30
GCA ATG TGG CTT TCT CGC TTG TTC ACA GTT TAC TGC TCT GCT CTG NNT    268
Ala Met Trp Leu Ser Arg Leu Phe Thr Val Tyr Cys Ser Ala Leu Xaa
      -25                                -20                                -15
GTT CTG CCT CTT CTT GGG TTG CAT GAA GCA GCA AGC TTT TAC CAA CGT    316
Val Leu Pro Leu Leu Gly Leu His Glu Ala Ala Ser Phe Tyr Gln Arg
      -10                                -5                                1                                5
GCT TTG CTG GCA AAT GCT CTT ACC AGT GCT CTG AGG CTG CAT CAA AGA    364
Ala Leu Leu Ala Asn Ala Leu Thr Ser Ala Leu Arg Leu His Gln Arg
      10                                15                                20
TTA CCA CAC TTC CAG TTA AGC AGA GCA TTC CTG GCC CAG GCT TTG TTA    412
Leu Pro His Phe Gln Leu Ser Arg Ala Phe Leu Ala Gln Ala Leu Leu
      25                                30                                35
GAG GAC AGC TGC CAC TAC CTG TTG TAT TCA CTC ATC TTT GTA AAT TCC    460
Glu Asp Ser Cys His Tyr Leu Leu Tyr Ser Leu Ile Phe Val Asn Ser
      40                                45                                50
TAT CCA GTT ACA ATG AGT ATC TTC CCA GTC TTG TTA TTC    499
Tyr Pro Val Thr Met Ser Ile Phe Pro Val Leu Leu Phe
      55                                60                                65

```

## (2) INFORMATION FOR SEQ ID NO: 189:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 45..221

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 1..177  
id HUMHBC4659  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 63..221

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 1..159  
id AAL60569  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 124..159

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 97..132  
id R88362  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 1..72

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5  
seq XVLVLSVVXXAMA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ATG CGT TTC CGC CAT TTT TGM AAA TWA ATT GGG MAG GTA CTG GTT TTA	48
Met Arg Phe Arg His Phe Xaa Lys Xaa Ile Gly Xaa Val Leu Val Leu	
-20 -15 -10	
AGT GTA GTT SCC GMC GCA ATG GCA GCC TTT GCA GTG SHA CCT CAG GGG	96
Ser Val Val Xaa Xaa Ala Met Ala Ala Phe Ala Val Xaa Pro Gln Gly	
-5 1 5	
CCC GCG TTA SSM TCT GAA CCA MTG MTG CYG GGT TCA CCC ACA TCT CCA	144
Pro Ala Leu Xaa Ser Glu Pro Xaa Xaa Xaa Gly Ser Pro Thr Ser Pro	
10 15 20	
AAG CCA GGA GTT AAT GCC CAG TTC TTA CCT GGA TTT TTA ATG GGG GMT	192
Lys Pro Gly Val Asn Ala Gln Phe Leu Pro Gly Phe Leu Met Gly Xaa	
25 30 35 40	

TTG CCA GCT CCG GTG ACT CCA CAA CCT  
Leu Pro Ala Pro Val Thr Pro Gln Pro  
45

219

## (2) INFORMATION FOR SEQ ID NO: 190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 105..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..310  
id T26956  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..359
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..315  
id T31666  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 202..332
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 137..267  
id R14990  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 127..201
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 63..137  
id R14990  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..50  
id R14990  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..120  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.2  
seq LCVEFASVASCDA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ATG GAG TTG GGG AGT TGC CTG GAG GGC GGG AGG GAG GCG GCG GAG GAA	48
Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu	
-40 -35 -30 -25	
GAG GGC GAG CCT GAG GTG AAA AAG CGG CGA CTT CTG TGT GTG GAG TTT	96
Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe	
-20 -15 -10	
GCC TCG GTC GCA AGC TGC GAT GCC GCA GTG GCT CAG TGC TTC CTG GCC	144
Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala	
-5 1 5	
GAG AAC GAC TGG GAG ATG GAA AGG GCT CTG AAC TCC TAC TTC GAG CCT	192
Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro	
10 15 20	
CCG GTG GAG GAG AGC GCC TTG GAA CGC CGA CCT GAA ACC ATC TCT GAG	240
Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu	
25 30 35 40	
CCC AAG ACC TAT GTT GAC CTA ACC AAT GAA GAA ACA ACT GAT TCC ACC	288
Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr	
45 50 55	
ACT TCT AAA ATC AGC CCA TCT GAA GAT ACT CAG CAA GAA AAT GGC AGC	336
Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser	
60 65 70	
ATG TTC TCT CTC ATT ACC TGG AAT ATT GAT GGA TTA GAT CTA AAC AAT	384
Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn	
75 80 85	
CTG TCA GAG AGG GCT CGA GGG GTG TGT TCC TAC TTA GCT TTG TAC AGC	432
Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser	
90 95 100	
CCA GAT GTG ATA TTT CTA CAG GAA GTT ATT CCC CCA TAT TAT AGC TAC	480
Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr	
105 110 115 120	
CTA	483
Leu	

## (2) INFORMATION FOR SEQ ID NO: 191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 182..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 165..384  
id W56608  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 30..115  
id W56608  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 127..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 111..175  
id W56608  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..446
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 385..430  
id W56608  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 311..446
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..136  
id R17248  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 13..378
- (C) IDENTIFICATION METHOD: Von Heijne matrix



(D) OTHER INFORMATION: score 5  
seq RLVVVSVSPQSGRA/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

```

AGTGCGGCCG TC ATG GCG TCG CCC TTC AGC GGG GCG CTG CAG CTG ACG GAC   51
      Met Ala Ser Pro Phe Ser Gly Ala Leu Gln Leu Thr Asp
      -120                               -115                   -110

CTG GAT GAC TTC ATC GGG CCG TCT CAG GAG TGC ATC AAG CCT GTC AAA   99
Leu Asp Asp Phe Ile Gly Pro Ser Gln Glu Cys Ile Lys Pro Val Lys
      -105                               -100                   -95

GTG GAA AAA AGG GCG GGA AGT GGC GTG GCC AAG ATT CGC ATT GAA GAT  147
Val Glu Lys Arg Ala Gly Ser Gly Val Ala Lys Ile Arg Ile Glu Asp
      -90                               -85                   -80

GAC GGG AGC TAC TTC CAA ATT AAC CAA GAC GGC DGG ACC CGG AGG CTG  195
Asp Gly Ser Tyr Phe Gln Ile Asn Gln Asp Gly Xaa Thr Arg Arg Leu
      -75                               -70                   -65

GAG AAG GCC AAG GTC TCG CTA AAC TAC TGC NWG GCG TGC AGC GGC TGC  243
Glu Lys Ala Lys Val Ser Leu Asn Tyr Cys Xaa Ala Cys Ser Gly Cys
      -60                               -55                   -50

ATC ACC TCC GCA GAG ACC GTG CTT ATC ACC CAG CAG AGC CAC GAG GAG  291
Ile Thr Ser Ala Glu Thr Val Leu Ile Thr Gln Gln Ser His Glu Glu
      -45                               -40                   -35                   -30

CTG AAG AAG GTT CTA GAT GCT AAC AAG ATG GCG GCA CCC AGT CAG CAG  339
Leu Lys Lys Val Leu Asp Ala Asn Lys Met Ala Ala Pro Ser Gln Gln
      -25                               -20                   -15

AGG CTG GTT GTA GTT TCG GTC TCA CCA CAG TCT AGA GCA TCG CTG GCT  387
Arg Leu Val Val Val Ser Val Ser Pro Gln Ser Arg Ala Ser Leu Ala
      -10                               -5                   1

GCA CGG TTT CAG CTG AAW CCT ACA GAT ACT GCC AGG AAA TTA ACC TCA  435
Ala Arg Phe Gln Leu Xaa Pro Thr Asp Thr Ala Arg Lys Leu Thr Ser
      5                               10                   15

TTC TTT AAA
Phe Phe Lys
20

```

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: DOUBLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..97
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 1..54  
id H30111  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 84..215
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq SLVAELLLGAGSG/SH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

```

ATACTTTCTG YAGYAGTCCT GGACCTCCTG TGCAAGAACA TGAAACACCT GTGGTTCATC      60
CTCCTGCTGG TGGCAGCTCC CAG ATG GGT CCT GTC CCG ACT GCA GTT GCA GGG      113
               Met Gly Pro Val Pro Thr Ala Val Ala Gly
                   -40                               -35

GCT GGC TCA CGA CTG GTA AAG CCC TCA CAG ACC CTG TCC CTC ACC TGC      161
Ala Gly Ser Arg Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys
                   -30                               -25                               -20

GCT GTC TCT GGT GGC TCA TTA GTA GCG GAA CTT CTT CTT GGA GCT GGA      209
Ala Val Ser Gly Gly Ser Leu Val Ala Glu Leu Leu Leu Gly Ala Gly
                   -15                               -10                               -5

TCC GGC AGT CAC CTG GGA CGG GCC TGG AGT GGA TTG GGT TCA TCT ATT      257
Ser Gly Ser His Leu Gly Arg Ala Trp Ser Gly Leu Gly Ser Ser Ile
                   1                               5                               10

ATA GAG GCA ATA GTG GGA GTA CTT CTT ACA ATC CGT CCC TCA AGA CTC      305
Ile Glu Ala Ile Val Gly Val Leu Leu Thr Ile Arg Pro Ser Arg Leu
                   15                               20                               25                               30

GAG CCA CCA TAT CAC TGG ACA AGC CCC GCG      335
Glu Pro Pro Tyr His Trp Thr Ser Pro Ala
                   35                               40

```

## (2) INFORMATION FOR SEQ ID NO: 193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 222..359  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 33..170  
                           id T50032  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 348..393  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 160..205  
                           id T50032  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 189..229  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..41  
                           id T50032  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 128..196  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.4  
                           seq QFILLGTTSVVTA/AL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

```

GACTGATTTC GAGTTTCCGG TCAGGTTAGG CCGGGGGGGT GCGGTCCTGG TCGGAAGGAG   60
GTGGAGAGTC GGGGGTCACC AGGCCTATCC TTGGCGCCAC AGTCGGCCAC CGGGGCTCGC   120
CGCCGTC ATG GAG AGC GGA GGG CGG CCC TCG CTG TGC CAG TTC ATC CTC   169
    Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu
          -20                      -15                      -10

CTG GGC ACC ACC TCT GTG GTC ACC GCC GCC CTG TAC TCC GTG TAC CGG   217
Leu Gly Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg
          -5                      1                      5

CAG AAG GCC CGG GTC TCC CAA GAG CTC AAG GGA GCT AAA AAA GTT CAT   265
Gln Lys Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His
          10                      15                      20

TTG GGT GAA GAT TTA AAG AGT ATT CTT TCA GAA GST CCA GGA AAA TGC   313
Leu Gly Glu Asp Leu Lys Ser Ile Leu Ser Glu Xaa Pro Gly Lys Cys
          25                      30                      35

GTG CCT TAT GCT GTT ATA GAA GGA GCT GTG CGG TCT GTT AAA GAA ACG   361
Val Pro Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr
          40                      45                      50                      55

```

CTT AAC ACC CAG TTT GTG GAA AAC TGC AAG  
Leu Asn Ser Gln Phe Val Glu Asn Cys Lys  
60 65

391

## (2) INFORMATION FOR SEQ ID NO: 194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 269..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..75  
id R33746  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 391..459
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 124..192  
id R33746  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 344..391
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 78..125  
id R33746  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 397..453
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq IYIICFXLPPLFS/FN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

ATATATAAAT GTTTCATGTT ATTGGTTTGG TACCTAGTCC TTTGCATGGA TATATAGGTA 60  
CCTAATGAAA ATCGAGGATC AGTGTATGAC AAATCTCCCA TCCTCCCCTT TCCTTATTGC 120

```

CTGTCTCGCC AATAGGAAGT AGAATAGTTG TGTGTTSTTT ACTTACTTST CTGTTTTAGA 180
GAGATTCTTA TTTTGGTAG GGAATATTC TAATATGTTT TCATATCTTT ATTTCATTTT 240
GTAGTCTTTT GCATGGCTAT GTAGGGACCT AATGAAAGTC GASTTTCATA ATATSACAGC 300
TCACDTCTTT TCCTACATAT TTCCTCACTT AGCAGTAGCT WGNKAGTTAT KTTSTGGTTA 360
TTTATTTCa TTCTCTAGGA TCTATTCCAT TIGNNG ATG CAA GTG TWT AGA TGC 414
                               Met Gln Val Cys Arg Cys
                               -15

ATA TAT ATC ATT TGC TTC TWT CTG CCG CCA TTA TTT TCC TTT AAC 459
Ile Tyr Ile Ile Cys Phe Xaa Leu Pro Pro Leu Phe Ser Phe Asn
      -10              -5              1

```

## (2) INFORMATION FOR SEQ ID NO: 195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..193
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96.1  
region 1..152  
id HSU78678  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 90..171  
id N41898  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 95..176  
id H69272  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 112..193  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 39..120  
 id N20619  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 44..88  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.1  
 seq QRLLLRFLASVIS/RK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```

GGGAGGGCTA GGCTGTGCAT CCCTCGCTC GCATTGCAGG GAG ATG GCT CAG CGA      55
                                   Met Ala Gln Arg
                                   -15

CTT CTT CTG AGG TTC CTG GCC TCT GTC ATC TCC AGG AAG CCC TCT CAR      103
Leu Leu Leu Arg Phe Leu Ala Ser Val Ile Ser Arg Lys Pro Ser Gln
-10                               -5                               1                               5

GGT CAG TGG GCC ACC CCT CAC TTC CAG AGC CCT GCA GAC CCC ACA ATG      151
Gly Gln Trp Ala Thr Pro His Phe Gln Ser Pro Ala Asp Pro Thr Met
                               10                               15                               20

CAG TCC TGG TGG CCT GAC TGT AAC ACC CAA CCC AGC CCG GAC              193
Gln Ser Trp Trp Pro Asp Cys Asn Thr Gln Pro Ser Pro Asp
                               25                               30                               35
  
```

## (2) INFORMATION FOR SEQ ID NO: 196:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 111..277  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 3..169  
 id AA149704  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 143..262  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq FLWLITRPQPVLPL/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```

AAGTCCTAGG AGCTGTGGAA AGAGTAGAAG TGCCTGAATG TGGTGCTGAA TCAATACAGC   60
CAGCTGTGAG GGGAGCACTT CCTGGACCCA GGAAGGGAGA GTCTTCTTCC AAGGTCTGAA   120
TTTCTGCTG CTGTTACAAA AG ATG CTT TTT ATC TTT AAC TTT TTG TTT TCC   172
                Met Leu Phe Ile Phe Asn Phe Leu Phe Ser
                -40                               -35

CCA CTT CCG ACC CCG GCG TTG ATC TGC ATC CTG ACA TTT GGA GCT GCC   220
Pro Leu Pro Thr Pro Ala Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala
-30                -25                               -20                               -15

ATC TTC TTG TGG CTG ATC ACC AGA CCT CAA CCC GTC TTA CCT CTT CTT   268
Ile Phe Leu Trp Leu Ile Thr Arg Pro Gln Pro Val Leu Pro Leu Leu
                -10                               -5                               1

GAC CTG AAC CKG   280
Asp Leu Asn Xaa
5

```

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 323..443  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 2..122  
 id R84934  
 est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 323..390  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 1..68  
 id AA020870  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 373..443  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 52..122  
                           id AA020870  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(407..438)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 42..73  
                           id AA187611  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 297..434  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
                           seq SHMLQLLPKALC/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```

TTTGTGGGCT CCTCTTTGGG GTGACCACTG CTTTCAAAGC CATCTGCCAA GGCTCTCCAG   60
GGCAGGACCT GACTGGTGGG GAATGAGTGT TCAGAAGCCT TGGGAGAGGC CAAAGAGCCA  120
TTCTAGGATG RTCKGAGGAA AACCTTCCTG CAGAGGCCAG AAACCTTGAG CTTAGGTGCC  180
TGGGGACCAG CTTCGACATT CTCTCCAGTT TCTGATTCTA ATTTTGGCCA CGTGTCACAA  240
CTTTTCCAGT CTCTGAGAAG GTCCCAGVCT TTCTCAAATA TTCTGATTTT GAAAAT ATG   299
                                         Met
TAT CCA AAG TGG GAG GCC CCT GTG ACA TTT TGC CAA CTT AAA CGA GAA   347
Tyr Pro Lys Trp Glu Ala Pro Val Thr Phe Cys Gln Leu Lys Arg Glu
-45                -40                -35                -30
AAA GAC CCC CCG CAC CCG GCA CAC TCC CCC TTC CTC CAG CCC CGC TTC   395
Lys Asp Pro Pro His Pro Ala His Ser Pro Phe Leu Gln Pro Arg Phe
-25                -20                -15
AGC CAC ATG CTC CAG CTG CTG CCC AGT AAA GCC CTG TGC CTT TTT TTC   443
Ser His Met Leu Gln Leu Leu Pro Ser Lys Ala Leu Cys Leu Phe Phe
-10                -5                1

```

## (2) INFORMATION FOR SEQ ID NO: 198:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 42..151

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: Identity 95  
region 1..110  
id AA121585  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: Identity 95  
region 101..172  
id AA121585  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 42..136

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..95  
id AA100539  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 100..171  
id AA100539  
est

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: 36..167

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7  
seq LAERLGLFEELWA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

ACTGTTTGAG GATGTAGGCA CTGGTGTGAA GGAAC ATG GCC CTG TAT CAG AGG 53  
Met Ala Leu Tyr Gln Arg  
-40

TGG CGG TGT CTC CGG CTC CAA GGT TTA CAG GCT TGC AGG CTA CAC ACG 101  
Trp Arg Cys Leu Arg Leu Gln Gly Leu Gln Ala Cys Arg Leu His Thr  
-35 -30 -25

```

GCA GTT GTG TCG ACC COT CCA CGC TGG TTG GCA GAG CGG CTT GGC CTT    149
Ala Val Val Ser Thr Pro Pro Arg Trp Leu Ala Glu Arg Leu Gly Leu
      -20                      -15                      -10

TTT GAG GAG CTG TGG GCT GCT CAG GTA AAG AGA TTA GCA AGC ATG GCA    147
Phe Glu Glu Leu Trp Ala Ala Gln Val Lys Arg Leu Ala Ser Met Ala
      -5                      1                      5                      10

CAG AAG GAA CCC CAG ACG                                          215
Gln Lys Glu Pro Gln Thr
              15

```

## (2) INFORMATION FOR SEQ ID NO: 199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 22..241  
id C16912  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 172..260
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 64..152  
id T68684  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..164
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 26..58  
id T68684  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig peptide
- (B) LOCATION: 93..166
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.8  
seq XGLLLFLLPGLG/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```

AGAGAGAGGA ACTGGGGTCT CCAGTCACGG GAGCCAGGAG CCGGCCAGGG CCCGAGSAGS   60
AAGGGAGCGA GGCTGAAGGG AACGTCGTCC TCTCAGC ATG GGG GTC CCG CGG CCT   115
                               Met Gly Val Pro Arg Pro
                               -20

CAG CCC TGG GCG STG GGG CTC CTG CTC TTT CTC CTT CCT GGG AGC CTG   163
Gln Pro Trp Ala Xaa Gly Leu Leu Leu Phe Leu Leu Pro Gly Ser Leu
      -15                      -10                      -5

GGG GCA GAA AGC CAC CTC TCC CTC CTG TAC CAC CTT ACC GCG GTG TCC   211
Gly Ala Glu Ser His Leu Ser Leu Leu Tyr His Leu Thr Ala Val Ser
      1                      5                      10                      15

TCG CCT GCC CCG GGG ACT CCT GCC TTC TGG GTG TCC GGC TGG CTG GGC   259
Ser Pro Ala Pro Gly Thr Pro Ala Phe Trp Val Ser Gly Trp Leu Gly
      20                      25                      30

CCG CAG CAG TAC CCG AGC CAG                               280
Pro Gln Gln Tyr Pro Ser Xaa
      35

```

## (2) INFORMATION FOR SEQ ID NO: 200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..249
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 5..252  
id C18087  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 166..350
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 20..204  
id AA018305  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 187..350  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
 region 42..205  
 id AA015592  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 181..350  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 33..202  
 id AA018631  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 150..181  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..32  
 id AA018631  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 158..338  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 12..192  
 id R93954  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 28..162  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 13.4  
 seq LVLALXLVSAALS/SV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```

AAGCGCAGGC TCCCAGCCGA GTCCGTT ATG GCC GCT GCC CTC CCG AAG AGG ATG   54
                        Met Ala Ala Ala Val Pro Lys Arg Met
                        -45                      -40

AGG GGG CCA GCA CAA GCG AAA CTG CTG CCC GGG TCG GCC ATC CAA GCC   102
Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln Ala
-35                      -30                      -25

CTT GTG GGG TTG GCG CGG CCG CTG GTC TTG GCG CTC VTG CTT GTG TCC   150
Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Xaa Leu Val Ser
-20                      -15                      -10                      -5

GCC GGT CTA TCC AGT GTT GTA TCA CCG ACT GAT TCA CCG AGC CCA ACC   198
Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro Thr
                        1                      5                      10

```

GTA CTC AAC TCA CAT ATT TCT ACC CCA AAT GTS AAT GGT TTA ACA CAT	246
Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr His	
15 20 25	
GAA AAC CAA ACC AAA CCT TCT ATT TCC CAA ATC ACC ACC ACC CTC CCT	294
Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu Pro	
30 35 40	
CCC AYT NCG AGT ACC AAG VNA AGT GGA GGA GCA TYT CTC GTC CCT CAT	342
Pro Xaa Xaa Ser Thr Lys Xaa Ser Gly Gly Ala Xaa Val Val Pro His	
45 50 55 60	
CCC TCG CCA GGG	354
Pro Ser Pro Gly	

## (2) INFORMATION FOR SEQ ID NO: 201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 170..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 117..269  
id HSC3DG011  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 1..132  
id HSC3DG011  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(177..209)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 337..369  
id H41589  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 137..223

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 13  
 seq LLLVLLLVTRXRS/MP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

AATTTGTGGC GCGCTGGTCC CCTCAGAGGG TTCCTGCTGC TCCGGGTGCC TTGGACCCTC   60
CCGCTCGCTT CSNGTTCTAC TGCCCCAGGA GCGCGGCGGG TCCGGGACTC CCGKCCGTGC   120
CGGTGCGGGC GCCGGC ATG TGG CTG TGG GAG GAC CAG GGC GGC CTC CTG GGC   172
          Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly
                               -25                -20

CCT TTC TCC TTC CTG CTG CTA GTG CTG CTG CTG GTC AGC CGG ASC CGG   220
Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Xaa Arg
      -15                -10                -5

TCA ATG CCT GCC TCC TCA CCG GCA GCC TCT TCG TTC TAC TGC GCG TCT   268
Ser Met Pro Ala Ser Ser Pro Ala Ala Ser Ser Phe Tyr Cys Ala Ser
      1                5                10                15

TCA GCT BTG AGC CGG TGC CCT CTT GCA GGG CCC TGC ACG TGC TCA AGC   316
Ser Ala Xaa Ser Arg Cys Pro Leu Ala Gly Pro Cys Arg Cys Ser Ser
          20                25                30

CCC GGG ACC GCA TTT CTG   334
Pro Gly Thr Ala Phe Leu
          35
  
```

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 281 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 24..280  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 28..284  
                           id R02745  
                           est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 3..176  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98

region 6..179  
id T84331  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 172..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 176..284  
id T84331  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..254  
id AA017512  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..254  
id N95074  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 173..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 146..253  
id N75564  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 65..151  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 40..126  
id N75564  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..66  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 1..40  
id N75564  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 36..119

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 11.6  
 seq LLLLVQLLRFLRA/DG

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```

ATTTCCTTCCC CCCGAGCTGG GCGTGCGCGG CCGCA ATG AAC TGG GAG CTG CTG      53
                               Met Asn Trp Glu Leu Leu
                               -25

CTG TGG CTG CTG GTG CTG TGC GCG CTG CTC CTG CTC TTG GTG CAG CTG      101
Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu Leu Leu Val Gln Leu
-20                               -15                               -10

CTG CGC TTC CTG AGG GCT GAC GGC GAC CTG ACG CTA CTA TGG GCC GAG      149
Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu Leu Trp Ala Glu
-5                               1                               5                               10

TGG CAG GGA CGA CGC CCA GAA TGG GAG CTG ACT GAT ATG GTG GTG TGG      197
Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp Met Val Val Trp
15                               20                               25

GTG ACT GGA GCC TCG AGT GGA ATT GGT GAG GAG CTG GCT TAC CAG TTG      245
Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu Ala Tyr Gln Leu
30                               35                               40

TCT AAA CTA GGA GTT TGT CTT GTG CTG TCA GCC AGG      281
Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg
45                               50

```

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 35..216  
id T86663  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97



region 43..158  
id AA055860  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 177..236  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 11.2  
seq AFLLLVALSYTLA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

AGAAGATAAT CACTTGGGGA AAGGAAGGTT CGTTTCTGAG TTAGCAACAA GTAAATGCAG 60  
CACTAGTGGG TGGGATTGAG GTATGCCCTG GTGCATAAAT AGAGACTCAG CTGTGCTGGC 120  
ACACTCAGAA GCTTGGACCG CATCCTAGCC GCCGACTCAC ACAAGGCAGA GTTGCC ATG 179  
Met  
-20  
GAA AAA ATT CCA GTG TCA GCA TTC TTG CTC CTT GTG GCC CTC TCC TAC 227  
Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Val Ala Leu Ser Tyr  
-15 -10 -5  
ACT CTG GCC AGA GAT ACC ACA GTC AAA CCT GGA GCC AAA AAG GAC ACA 275  
Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp Thr  
1 5 10  
AAG GAC TCT CGA CCC AAA CTG CCC CAG ACC CTC TCC AGA GGT TGG GGT 323  
Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly  
15 20 25  
GAC CAA CTC ATC TGG ACA CGG 344  
Asp Gln Leu Ile Trp Thr Arg  
30 35

## (2) INFORMATION FOR SEQ ID NO: 204:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 171..312  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 33..174  
id T86663

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 171..288
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 41..158  
id AA055880  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 127..246
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2  
seq AFLLLVALSYTLA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

```
AAGATTACAC AGGCCAACAG ACAACCCAAA GTCATTAAGC CATGAGAGTG GAATGAATCT   60
ATGAAAACTC AATGAAGACA GAACAAGAGA AAAATCTTTT CAGCCACGAT GAATTAGGRG  120
ACAAG ATG TCA AAT TAC ACT GAT GCT GAG TCA ACC TTC TCA AAG CAA   168
Met Ser Asn Tyr Thr Asp Ala Glu Ser Ser Phe Ser Lys Gln
-40 -35 -30
GAG ATA ATC AGA GTT GCC ATG GAG AAA ATT CCA GTG TCA GCA TTC TTG   216
Glu Ile Ile Arg Val Ala Met Glu Lys Ile Pro Val Ser Ala Phe Leu
-25 -20 -15
CTC CTT GTG GCC CTC TCC TAC ACT CTG GCC AGA GAT ACC ACA GTC AAA   264
Leu Leu Val Ala Leu Ser Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys
-10 -5 1 5
CCT GGA GCC AAA AAG GAC ACA AAG GAC TCT CGA CCC AAA CCG CCC CGG   312
Pro Gly Ala Lys Lys Asp Thr Lys Asp Ser Arg Pro Lys Pro Pro Arg
10 15 20
```

## (2) INFORMATION FOR SEQ ID NO: 205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 96..165
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 364..433  
id AA100852  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 314..364  
id AA100852  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 14..46  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 282..314  
id AA100852  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 96..202  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 65..171  
id AA113841  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 31..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..65  
id AA113841  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 290..324  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 326..360  
id AA133048  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 158..191  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 2..35  
id AA133048  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 169..290  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..122  
                           id AA159272  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 53..95  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 323..365  
                           id AA161042  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 96..138  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 365..407  
                           id AA161042  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 14..46  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 282..314  
                           id AA161042  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 3..161  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 10.6  
                           seq FILLLIFIAEVAA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

AC ATG CAG TTT GNA ACG TGG GCT ACT TCC TCA TCG CAG CCG GCG TTG	47
Met Gln Phe Xaa Thr Trp Ala Thr Ser Ser Ser Gln Pro Ala Leu	
-50 -45 -40	
TGG TCT TTG CTC TTG GTT TCC TGG GCT GCT ATG GTG CTA AGA CTG AGA	95
Trp Ser Leu Leu Leu Val Ser Trp Ala Ala Met Val Leu Arg Leu Arg	
-35 -30 -25	
AGC AAG TGT GCC CTC GTG ACG TTC TTC TTC ATC CTC CTC ATC TTC	143
Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile Phe	
-20 -15 -10	
ATT GGT GAG GTT GCA GCT GCT GTG GTC GCC TTG GTG TAC AAC ACA ATG	191
Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Xaa Thr Met	
-5 1 5 10	
BDT GAG CAG TTC CTG ACG TTG CTC GTA GTG GCT GCC ATC AAG AAA GAT	239

```

Xaa Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys Asp
      15              20              25

TAT GGT TCC CAG GAA GAC TTC ACT CAA GTG TGG AAC ACC ACC ATG AAA      287
Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Xaa Asn Thr Thr Met Lys

      30              35              40

GGG CTC AAG TGC TGT GGC TTC ACC AAC TAT ACG GAC TGG      326
Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Trp

      45              50              55

```

## (2) INFORMATION FOR SEQ ID NO: 206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 147..283  
id N36076  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..140
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 40..148  
id N36076  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 287..333
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 296..342  
id N36076  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..33
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 8..40  
id N36076

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..333  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 9..340  
id N95074  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..333  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 9..340  
id AA017512  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 140..333  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 146..339  
id W04626  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 5..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 12..147  
id W04626  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..334  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 47..336  
id H27747  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 1..34  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..34  
id H27747  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 3..36  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.5

seq LLLLVHLLRFLRA/DG

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```

AA ATG AAC TGG CAG CTG CTG CTG TGG CTG CTG GTG CTG TGC GCG CTG      17
Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu
      -25                      -20                      -15

CTC CTG CTC TTG GTG CAT CTG CTG CGC TTC CTG AGG GCT GAC CGC GAC      95
Leu Leu Leu Leu Val His Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp
      -10                      -5                      1

CTG ACC CTA CTA TGG GCC GAG TGG CAG GGA CGA CGC CCA GAA TGG GAG     143
Leu Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu
      5                      10                      15

CTG ACT GAT ATG GTG GTG TGG GTG ACT GGA GCC TCG AGT GGA ATT GGT     191
Leu Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly
      20                      25                      30                      35

GAG GAG CTG GGT TAC CAG TTG TCT AAA CTA GGW KTT TCT CTT GTG CTG     239
Glu Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Xaa Ser Leu Val Leu
      40                      45                      50

TCA GCC AGA AGA GTG CAT GAG CTG GAA AGG GTG AAA AGA AGA TGC CTA     287
Ser Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu
      55                      60                      65

GAG AAT GGC AAT TTA ARA GAA AAA GAT ATA CTT GTT TTG CCC CTT GGG     335
Glu Asn Gly Asn Leu Xaa Glu Lys Asp Ile Leu Val Leu Pro Leu Gly
      70                      75                      80

```

(2) INFORMATION FOR SEQ ID NO: 207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 424..533  
id N80896  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(283..318)

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 342..377  
 id W16973  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 293..347  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..55  
 id R02710  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 120..272  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 10.3  
 seq VSCLTLWSPGCW/PQP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

```

TGCACIATGC TTGTGTGTAT GTGTGTGCCT CTGTCTTGCT CTCTTATCTC CCAGCAGTGA    60
GACATTGGAC GTSTTTGCTC ATGAAGATGC AGTATATGGC TTGTCTGTGA GCCCASTGA    119
ATG ACA ACA TTT TTG CCA GTT CCT CAG ATG ATG GCC GGG TTC TCA TTT    167
Met Thr Thr Phe Leu Pro Val Pro Gln Met Met Ala Gly Phe Ser Phe
-50                      -45                      -40

GGG ACA TTC GSG AAT CCC CCC ATG GAG AGC CCT TCT GCC TGG CAA ACT    215
Gly Thr Phe Gly Asn Pro Pro Met Glu Ser Pro Ser Ala Trp Gln Thr
-35                      -30                      -25                      -20

ATC CAT CAG CCT TTC ATA GTG TCA TGT TTA ACC CTG TGG AGC CCA GGT    263
Ile His Gln Pro Phe Ile Val Ser Cys Leu Thr Leu Trp Ser Pro Gly
-15                      -10                      -5

TGT TGG CCA CAG CCA ATT CAA AGG AAG GAG TGG GAC TCT GGG ACA TTC    311
Cys Trp Pro Gln Pro Ile Gln Arg Lys Glu Trp Asp Ser Gly Thr Phe
1                      5                      10

GAA AAC CTC AGA GTT CTC TCC TGC GCT ATG GTG GAA    347
Glu Asn Leu Arg Val Leu Ser Cys Ala Met Val Glu
15                      20                      25

```

## (2) INFORMATION FOR SEQ ID NO: 208:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA



## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 168..461  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 47..340  
id N39924  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 169..370  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 178..379  
id R61601  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 359..431  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 369..441  
id R61601  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 75..158  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.5  
seq LVXFSL LATAILG/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

ACCATAGCAA ATTAAATGAC TGCCATAAAG TATATTTTAC TCACAGGACA GATTACAATA    60
GCCTTGATAG AATC ATG GCA TCC AAA GGG ATG CGC CAT TTT TCC TTG ATT    110
      Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile
      -25                               -20

TCA GAG CAG TTG GTG TYC TTT AGT CTT CTT GCA ACA GCG ATT TTG GGA    158
Ser Glu Gln Leu Val Xaa Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly
-15                               -10                               -5

GCA GTT TCC TGG CAG CCA ACA AAT GGA ATT TTC TTG AGC ATG TTT CTA    206
Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu
  1              5              10              15

ATC GTT TTG CCA TTG GAA TCC ATG GCT CAT GGG CTC TTC CAT GAA TTG    254
Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu
      20              25              30

GGT AAC TGT TTA GGA GGA ACA TCT GTT GGA TAT GCT ATT GTG ATT CCG    302
G y Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro

```

35	40	45	
ACC AAC TTC TGC AGT CCT GAT GGT CAG CCA ACA CTG CTT CCC CCA GAA			350
Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu			
50	55	60	
CAT GTA CAG GAG TTA AAT TTG AGG TCT ACT GGC ATG CTC AAT GCT ATC			398
His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile			
65	70	75	80
CAA AGA TTT TTT GCA TAT CAT ATG ATT GAG ACC TAT GGA TGT GAC TAT			446
Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr			
85	90	95	
TCC ACA AGT GGA CTG			461
Ser Thr Ser Ser Gly Leu			
100			

## (2) INFORMATION FOR SEQ ID NO: 209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(31..239)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 3..211  
id N27605  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..111)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..110  
id N78549  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 78..140
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq VLPVILLLLGAHP/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```

AAGAGCAGAG CCGGAAGAAG GCGGGACGAA CCGGAASAGG GTGAAATGCT TTCGGTAGGC      60
ACTCCACGGC TGTGAAG ATG GCG GCG GCT GCG TGG CTT CAG GTG TTG CCT      110
      Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro
      -20                      -15

GTC ATT CTT CTG CTT CTG GGA GCT CAC CCG TCA GGA CTG TCG TTT TTC      158
Val Ile Leu Leu Leu Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe
-10                      -5                      1                      5

AST GCG GGA CCG GCA ACC GTA GCT GCT GCC GAC CCG TCC AAA TGG CAC      206
Ser Ala Gly Pro Ala Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His
      10                      15                      20

RKT CCG ATA CCG TCG GGG AAA AAT TAT TTT AGT TTT GGA AAG ATC CTC      254
Xaa Pro Ile Pro Ser Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu
      25                      30                      35

TTC AGA AAT ACC ACT ATC TTC CTG AAG TTT GAT GGA GAA CGA      296
Phe Arg Asn Thr Thr Ile Phe Leu Lys Phe Asp Gly Glu Arg
      40                      45                      50

```

## (2) INFORMATION FOR SEQ ID NO: 210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..281
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 78..241  
id R57572  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..91
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..54  
id R57572  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..122
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 52..84  
id R57572  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 117..272  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 59..214  
id W55468  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 273..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 214..269  
id W55468  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 130..456  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.1  
seq LVLAVLFFHQLVG/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```

ACTTTGTCAT TCAGCTGCCT GCTGCCTCCG CAGCGTCCCC CCAGCTCTCC CTGTGCTAAC   60
TGCTTGCACC TTGGACAGAG CGGGTCCGCA AATCAGAAGG ATTAGTTGGG ACCTGCCCTT   120
GGCGACCCC ATG GCA TCC CCC AGA ACC GTA ACT ATT GTG GCC CTC TCA GTG   171
Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val
-105 -100

GCC CTG GGA CTC TTC TTT GTT TTC ATG GGG ACT ATC AAG CTG ACC CCC   219
Ala Leu Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro
-95 -90 -85 -80

AGG CTC ACC AAG GAT GCC TAC AGT GAG ATG AAA CGT GCN NAC AAG AGC   267
Arg Leu Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Xaa Lys Ser
-75 -70 -65

TAT GTT CGA GCC CTC CCT CTG CTG AAG AAA ATG GGG ATC AAT TCC ATT   315
Tyr Val Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile
-60 -55 -50

CTC CTC CGA AAA AGC ATT GGT CCC CTT GAA GTG GCC TGT GGC ATC GTC   363
Leu Leu Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val
-45 -40 -35

ATG ACC CTT GTG CCT GGG CGT CCC AAA GAT GTG GCC AAC TTC TTC CTA   411
Met Thr Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu
-30 -25 -20

```

CTG TTG CTG GTG TTG GCT GTG CTC TTC TTC CAG CAG CTG GTC GST GAT 459  
Leu Leu Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp  
-15 -10 -5 1  
  
CCT CTC AAA 468  
Pro Leu Lys

## (2) INFORMATION FOR SEQ ID NO: 211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 84..217  
id AA021055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..70  
id AA021055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 84..217  
id W98068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..70  
id W98068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 88..191  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 11..114  
id AA059040  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 91..204  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.8  
seq LLLLCALHSHIYC/IK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```
CATAAAATTT GAGGATATCA GCTGATTATT TTTTCTTCCM ASAATGAAAA TCAAGCAGAA    60
TTGATTCCTA CACGAAAAAA AAGCACACGA ATG CCA AAC CTT TCC TTT GGT GGA    114
                               Met Pro Asn Leu Ser Phe Gly Gly
                               -35

CTG GAC ACT AAC CAG ATG AGA GTA AAT TTC TTA TCC GTG GAC GTA TGT    162
Leu Asp Thr Asn Gln Met Arg Val Asn Phe Leu Ser Val Asp Val Cys
-30                -25                -20                -15

AAG CTA CTG CTG CTG TGT GCT CTC CAC AGC CAT ATT TAT TGT ATT AAA    210
Lys Leu Leu Leu Leu Cys Ala Leu His Ser His Ile Tyr Cys Ile Lys
                -10                -5                1

CAA TCA GCA CTT CGG                                225
Gln Ser Ala Leu Arg
5
```

## (2) INFORMATION FOR SEQ ID NO: 212:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 134..378  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 115..359  
id R67703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 23..135  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 5..117  
id R67703  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 134..318  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 115..299  
id H42383  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 20..135  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 2..117  
id H42383  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..383  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 87..277  
id W90193  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 134..192  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 29..87  
id W90193  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 417..454  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 314..351  
id W90193  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 288..470  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..183  
id R53752  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 258..422
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq XXLLLLNVGQLLA/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

AACCCACGGT GGGGGGAGCG CGGCCATGGC GTCCTGCTT TCGGTGCTGC GTGTACTGCT   60
GGGCGGCTTC TTCGCGCTCG TGGGGTTGGC CAAGCTCTCG GAGGAGATCT CGGCTCCAGT  120
TTGGGAGCGG RTGRAATGCC CTGTTCGTGC AGTTTGCTGA TGTGTTCCCG CTGAAGGTAT  180
TTGGCTACCA GCCAGATCCC CTGAAGTACC AAATAGCTGT GGGCTTTCTG GAACTGCTGG  240
CTGGGTTGCT GCTGGTC ATG GGC CCA CCG ATG CTG CAA GAG ATC AGT AAC   290
      Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn
      -55                      -50                      -45

TTG TTC TTG ATT CTG CTC ATG ATG GGG GCT ATC TTC ACC TTG GCA GCT   338
Leu Phe Leu Ile Leu Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala
      -40                      -35                      -30

CTG AAA GAG TCA CTA AGC ACC TGT ATC CCA GCC ATT GTC TGC CTG NGG   386
Leu Lys Glu Ser Leu Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Xaa
      -25                      -20                      -15

TDN CTG CTG CTG CTG AAT GTC GGC CAG CTC TTA GCC CAG ACT AAG AAG   434
Xaa Leu Leu Leu Leu Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys
      -10                      -5                      1

GTG GTC AGA CCC ACT AGG AAG AAG ACT CTA AGT ACA   470
Val Val Arg Pro Thr Arg Lys Lys Thr Leu Ser Thr
      5                      10                      15

```

## (2) INFORMATION FOR SEQ ID NO: 213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 4..55
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 19..70



id T18977  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 141..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 157..211  
id T18977  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 92..137  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 109..154  
id T18977  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 245..355  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..111  
id HSC12A111  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 321..355  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..35  
id W73324  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 133..345  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq VVXFLLLXALIA/TY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

```
AAGCAGCTTC CAGGATCCTG AGATCCGGAG CAGCCGGGGT CGGAGCGGCT CCTCAAGAGT    60
TACTGATCTA TNNATGGCAG AGAAAAAAAA ATTGTGACCA GAGACGTGTA GCAATGAACA    120
AGGAACRTCA TA ATG RWN NNK TTC ACA GAC CCC TCT TCA GTG AAT GAA AAG    171
      Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys
      -70                      -65                      -60

AAG AGG AGG GAG CGG GAA GAA AGG CAG AAT ATT GTC CTG TGG AGA CAG    219
Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln
      -55                      -50                      -45
```

CCG CTC ATT ACC TTG CAG TAT TTT TCT CTG GAA ATC CTT GTA ATC TTG	267
Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu	
-40 -35 -30	
AAG GAA TGG ACC TCA AAA TTA TGG CAT CGT CAM MGC ATT GTG GTG WCT	315
Lys Glu Trp Thr Ser Lys Leu Trp His Arg Xaa Xaa Ile Val Val Xaa	
-25 -20 -15	
TTT TTA CTG CTG CTT GGT DGG CTT ATA GCT ACG TAT TAT	354
Phe Leu Leu Leu Leu Ala Xaa Leu Ile Ala Thr Tyr Tyr	
-10 -5 1	

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(2x) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 189..311  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 75..197  
id AA021160  
est

(1X) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 249..293  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq LLRGLLWXQVLCA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

ACCTTTCTGG GTTGAGCATG GCTGAAGTGA CTCAGCCCAT GGGAGGTTTC CTAGGAGNAA	60
CAGGCTCCAC TTGCTGCCTC TCTGCGTGAA CTCGGTGTGC CGGCAACCTG GCGACCAGAC	120
TCCTGCCTTC GGAGGGGCTG GGGCTCCAGG ACGTGAGTGC CCCCCRNKGT TGGAAGGCGG	180
TGTCATATGT GCACAGAAGC CAAAAAGCAT TGCTGGTATT TCGAAGGACT CTATCCAACC	240
YHPTATAT ATG CCG CTC CTA CGA GGA CTG CTG TGG STC CAG GTG CTG TGT	290
Met Pro Leu Leu Arg Gly Leu Leu Trp Xaa Gln Val Leu Cys	
-15 -10 -5	
GGG GGC CCT CTC CAT ACA GAG	311
Ala Gly Pro Leu His Thr Glu	

1

5

## (2) INFORMATION FOR SEQ ID NO: 215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 31..265  
id T78247  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 6..240  
id W17118  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 11..245  
id N88433  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 32..247  
id R35014  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 9..217  
id AA074562

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 159..218
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.4  
seq AVVGGCLLVPPAEA/NK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```

AAGAGGCGGA GATGGCGGAG GGCGGTGGGA CGTGATGCGC GGGTCAGAGC CGGGCCTTGA    60
GAAGGAACTG GAGGCCCTTG GCAGCGGTGT CCCCTCGAGG ACCCCTCTGC CGGGCTCACC    120
AGGTGTCCGG CTTTGCTGGC CCAGCAAGCC TGATAAGC ATG AAG CTC TTA TCT TTG    176
                               Met Lys Leu Leu Ser Leu
                               -20                               -15

GTG GCT GTG GTC GGG TGT TTG CTG GTG CCC CCA GCT GAA GCC AAC AAG    224
Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys
                -10                -5                1

AGT TCT GAA GAT ATC CRG TGC AAA TGC ATC TGT CCA CCT TAT AGA AAC    272
Ser Ser Glu Asp Ile Xaa Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
                5                10                15

ATC AGT GGG CAC ATT TAC AAC CAG AAT GTA TCC CAG AAG GAC TGC AAC    320
Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
                20                25                30

TGC CTG CAC GTG GTG GAG CCC ATG CCA GTG CCG    353
Cys Leu His Val Val Glu Pro Met Pro Val Pro
    35                40                45

```

## (2) INFORMATION FOR SEQ ID NO: 216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..332  
id HUM085F04B  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 139..249  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 187..297  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 249..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 295..368  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..148  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 133..195  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 80..264  
id R77008  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 94..327  
id H49758  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 53..237  
id AA056366  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 114..185  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```

AATTGGCTGG CTCTGSAAGC GCAGGTGGTC CTTCTTCTAC TGTCACATGG TGC GCGCTGT 80
TTTCTAATCA CGKGGGTGCC ACCCAGGCCT CTCTGCTCCT GTCKTKTGTT TGG ATG 116
                                         Met
CCG GCG CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC 164
Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val
          -20                      -15                      -10
TTG CTG ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC 212
Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala
          -5                      1                      5
TCG GAT TCC GGC TCT GGC TAC GTT CCG GGC TCG GTC TCT GCA GCC TTT 260
Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe
  10                      15                      20                      25
GTT ACT TGC CCC AAC GAG AAG GTC GCC AAG GAG ATC GCC AGG GCC GTC 308
Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala Val
          30                      35                      40
GGG GAG AAG CCG 320
Gly Glu Lys Arg
          45

```

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 73..333  
id H95186  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..133
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 25..86  
id H95186  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 28..351
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLGLLSAEQLAEA/SV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

```

ACGGGTGCCG GGTGGAGCGA ASACGGA ATG TGT CTC CTG CTG GGG GCC ACG GGC    54
                        Met Cys Leu Leu Leu Gly Ala Thr Gly
                        -105                      -100

GTC GGG AAG ACG CTG CTG GTG AAA CGG CTG CAG GAG GTG AGC TCC CGG    102
Val Gly Lys Thr Leu Leu Val Lys Arg Leu Gln Glu Val Ser Ser Arg
      -95                      -90                      -85

GAT GGG AAA GGC GAC CTG GGG GAG CCG CCG CCG ACA CCG CCC ACG GTG    150
Asp Gly Lys Gly Asp Leu Gly Glu Pro Pro Pro Thr Arg Pro Thr Val
      -80                      -75                      -70

GGC ACC AAT CTT ACT GAC ATC GTG GCA CAG AGA AAG ATC ACC ATC CGG    198
Gly Thr Asn Leu Thr Asp Ile Val Ala Gln Arg Lys Ile Thr Ile Arg
      -65                      -60                      -55

GAG CTT GGG GGG TGC ATG GGC CCC ATC TGG TCC AGT TAC TAT GGA AAC    246
Glu Leu Gly Gly Cys Met Gly Pro Ile Trp Ser Ser Tyr Tyr Gly Asn
      -50                      -45                      -40

TGC CGT TCT CTC CTG TTT GTG ATG GAC GCC TCT GAC CCC ACC CAG CTC    294
Cys Arg Ser Leu Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu
      -35                      -30                      -25                      -20

TCT GCA TTM SGT GTG CAG CTC TTA GGT CTC CTT TCT GCA GAA CAA CTT    342
Ser Ala Xaa Xaa Val Gln Leu Leu Gly Leu Leu Ser Ala Glu Gln Leu
      -15                      -10                      -5

GCA GAA GCA TCG GTG CTG ATA CTC TTC AAT AAA ATC GAC AAC    384
Ala Glu Ala Ser Val Leu Ile Leu Phe Asn Lys Ile Asp Asn
      -1                      5                      10

```

## (2) INFORMATION FOR SEQ ID NO: 218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 94..197  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 92..195  
id T93931  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..45  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..44  
id T93931  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..97  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 52..96  
id T93931  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 190..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 187..231  
id T93931  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 138..196  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 241..299  
id N25481  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 190..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 292..336  
id N25481  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 94..211  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 65..182  
id W19370  
est



## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 94..196  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 56..158  
id N35539  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 190..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 151..195  
id N35539  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 56..97  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 19..60  
id N35539  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 94..193  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 96..195  
id W87436  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..49  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 7..54  
id W87436  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 75..197  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.7  
seq LLCLGQLHHPGLG/RV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

AAAGTTTGTT CCCCAGATTG GGAGCCTAGG AGCCCCCGGC GGCTGCGGCG CAGGTGCCCT 60  
CGGCCTTAGT CGGG ATG GAG CTG CCT GCK GTG AAC CTT GAA AGT GAT TCT 110  
Met Glu Leu Pro Ala Val Asn Leu Glu Ser Asp Ser  
-40 -35 -30

CCT AGG TCA CTG GCT GCT GAC AAC CTG GGG CTG CAT TGT ATT CTC AGG	158
Pro Arg Ser Leu Ala Ala Asp Asn Leu Gly Leu His Cys Ile Leu Arg	
-25 -20 -15	
CTC CTA TGC CTG GGC CAA CTT CAC CAT CCT GGC CTT GGG CGT GTG GGC	206
Leu Leu Cys Leu Gly Gln Leu His His Pro Gly Leu Gly Arg Val Gly	
-10 -5 1	
TGT GGC TCA GCG GGA CTC CAT CGA CGC CGG	236
Cys Gly Ser Ala Gly Leu His Arg Arg Arg	
5 10	

## (2) INFORMATION FOR SEQ ID NO: 219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 99..194  
id N28787  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..95  
id N28787  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 207..280  
id N28787  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 114..208

WO 99/06550

198

id AA102327  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 30..110  
id AA102327  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..33  
id AA102327  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 277..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 250..284  
id AA102327  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 101..196  
id AA019783  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 209..282  
id AA019783  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 37..97  
id AA019783  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 115..210  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 41..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 13..111  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 253..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 223..289  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 145..240  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 102..197  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 253..326  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 210..283  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 75..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 34..98  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 171..323  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq PALILLFALGSLG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

AAATTTTCCT CCGGAAGTG CCGAGGAGGC GGTTCGGTT AGTGGACCGG GACCGGTAGG 60

```

GGTCCTGTTG CCATCATGGC TGACCCCGAC CCCCGGTAGC CTCGCTCCTC GATCGAGGAC 120
GACTTCAACT ATGGCAGCAA GCGTKGGCYT CAGGCAACCGT GCACATCCGA ATG GCC 176
                                         Met Ala
                                         -50

TTT CTG AGA AAA GTC TAC AGC ATT CTT TCT CTG CAG GTT CTC TTA ACT 224
Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu Thr
      -45                      -40                      -35

ACA GTG ACT TCA ACA GTT TTT TTA TAC TTT GAG TCT GTA CGG ACA TTT 272
Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Gln Ser Val Arg Thr Phe
      -30                      -25                      -20

GTA CAT GAG AGT CCT GCC TTA ATT TTG CTG TTT GCC CTC GGA TCT CTG 320
Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly Ser Leu
      -15                      -10                      -5

GGT TCG GGG 329
Gly Ser Gly
1

```

## (2) INFORMATION FOR SEQ ID NO: 220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..180  
id W88492  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 25..111
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq PTLAIALAANAWA/FV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

ACCATATGGG TGGTGTGGAT CGTC ATG TAT ACT TAC GGC AAC AAG CAG CAC 51
Met Tyr Thr Tyr Gly Asn Lys Gln His
      -25

```

```

AAC AGT CCC ACC TGG GAT GAC CCC ACG CTG SCC ATC GCC CTC GCC GCC      99
Asn Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala
-20                      -15                      -10                      -5

AAT GCC TGG GCC TTC GTC CTC TTC TAC GTC ATC CCC GAG GTC TCC CAG      147
Asn Ala Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln
                      1                      5                      10

GTG ACC AAG TCC AGC CCA GAG CAA AGC TAC CAG GGG GAC ATG TAC CCC      195
Val Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro
                      15                      20                      25

ACC CGG GAC TTG                                                    207
Thr Arg Asp Leu
                      30

```

## (2) INFORMATION FOR SEQ ID NO: 221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(136..167)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 239..270  
id H62766  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 70..165
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq WILVLALPLTVWP/WL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```

ACTTTCAGTT TCCTTCTTCC AGCACGGAGT ACACTGCTCT GCCTCCACTT AGATTACTTC      60

AGAAATGAA ATG CAG CAA ATA TTT ATC CAG CAG TGC AGG GAG TTG AAC TTT      111
Met Gln Gln Ile Phe Ile Gln Gln Cys Arg Glu Leu Asn Phe
                      -30                      -25                      -20

TGG AGT CGG GAA CCT TGG ATT CTT GTT CTG GCT CTG CCA CTT ACT GTG      150
Trp Ser Arg Glu Pro Trp Ile Leu Val Leu Ala Leu Pro Leu Thr Val
                      -15                      -10                      -5

```

TGG GCT TGG CTC TCC CCG GAG GCT CAG CCC GGT CTG  
Trp Pro Trp Leu Ser Pro Glu Ala Gln Pro Pro Leu

195

## (2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 308..370  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 404..466  
id AA158879  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 110..154  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.5  
seq AVLLALLMAGLAL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

AACTGGCTCC AGGAAACCCG CTGGTGTGA CTGTGGGCG TCGAGCCTCT CCCCATTTGA 60

GGCCATATAA ANNACCTGAG GCCCTCTCCA CCACAGCCCA CCAGTGACC ATG AAG GCT 118  
Met Lys Ala  
-15

GTG CTG CTT GCC CTG TTG ATG GCA GGC TTG GCC CTG CAG CCA GGC ACT 166  
Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln Pro Gly Thr  
-10 -5 1

GCC CTG CTG TGC TAC TCC TGG ARR GCC CAG GTG RGC AAC GAG GAC TGC 214  
Ala Leu Leu Cys Tyr Ser Trp Xaa Ala Gln Val Xaa Asn Glu Asp Cys  
5 10 15 20

CTG CAG GTG GAG AAC TGC ACC CAG CTG GGG GAG CAG TGC TGG ACC GCG 262  
Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys Trp Thr Ala  
25 30 35

CGC ATC CGC GCA GTT GGC CTC CTG ACC GTC ATC AGC AAA GGC TGC AGC 310  
Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys Gly Cys Ser  
40 45 50

TTG AAC TGC GTG GAT SAC TCA CAG GAC TAC TAA GTG GGC AAG AAG AAC 358  
 Leu Asn Cys Val Asp Xaa Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn  
           55                                60                                65

ATC ACG TGC TGT GAC 373  
 Ile Thr Cys Cys Asp  
           70

## (2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
                           region 1..247  
                           id AAL66578  
                           est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 4..51
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
                           seq QACLLGLFALILS/GK

## -(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

AGA ATG GGA CTC CAA GCC TGC CTC CTA GCG CTC TTT GCC CTC ATC CTC 48  
 Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu  
       -15                                -10                                -5

TCT GGC AAA TGC AGT TAC AGC CCG GAG CCC GAC CAG CGG AGG ACG CTG 96  
 Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu  
       1                                5                                10                                15

CCC CCA GGC TGG GTG TCC CTG GGC CGT GCG GAC CCT GAG GAA GAG CTG 144  
 Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu  
                                 20                                25                                30

AGT CTC ACC TTT GCC CTG AGA CAG CAG AAT GTG GAA AGA CTC TCG GAG 192  
 Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu  
                                 35                                40                                45

CTG GTG CAG GGT GTG TCG GAT CCC AGC TCT CCT CAA TAC CGA AAA TAC 240



Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr  
50 55 60

CTG ACC GGT  
Leu Thr Arg  
65

249

## (2) INFORMATION FOR SEQ ID NO: 224:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (11) MOLECULE TYPE: CDNA

## (71) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(141..361)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 146..366  
id H19708  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 143..264  
id H20045  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 4..77  
id H20045  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 8..247  
id C15772  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 157..341  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 1..185  
                           id H67240  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 340..382  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 185..227  
                           id H67240  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 172..382  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..211  
                           id HUM408E11B  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 2..88  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7  
                           seq LGSGGLGLSPGTSS/GR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

G ATG AGG CCG GGG CAG GTC TCC CTC CTG GGT CCT GAT GCT GTT TCT GTG	49
Met Arg Pro Gly Gln Val Ser Leu Leu Gly Pro Asp Ala Val Ser Val	
-25 -20 -15	
CTC GGC TCT GGC TTG GGC CTC AGC CCT GGC ACC AGC TCT GGC CGC AAC	97
Leu Gly Ser Gly Leu Gly Leu Ser Pro Gly Thr Ser Ser Gly Arg Asn	
-10 -5 1	
CCT GAC CCT GGC TCT GGG CCG GGC ACT CTG CCG GRT YCC AGC DTC CAA	145
Pro Asp Pro Gly Ser Gly Pro Gly Thr Leu Pro Xaa Xaa Ser Xaa Gln	
5 10 15	
ARG CCC TCC CCG GCT CCA GAT CCA CCC CCA GCC CTA CTC CTG TGG AAT	193
Arg Pro Ser Pro Ala Pro Asp Pro Pro Pro Ala Leu Leu Leu Trp Asn	
20 25 30 35	
CTT CTG ACC CAA AGG CTG GGC ACG ACG CTG CTC CCG ACC TTG TGC CCA	241
Leu Leu Thr Gln Arg Leu Gly Thr Thr Leu Val Pro Thr Leu Cys Pro	
40 45 50	
GGG CAG ACC TTG ATC CTG TGC CCA GCC CAG ACC CTG ATC CTG TGC CCA	289
Ala Gln Thr Leu Ile Leu Cys Pro Ala Gln Thr Leu Ile Leu Cys Pro	
55 60 65	
ACC CTG ATC CCA ACC CTG TGT CCT GCC CTG AAC CCT GTT CTC CCA CTC	337
Xaa Leu Ile Pro Thr Leu Cys Pro Ala Leu Xaa Pro Val Leu Pro Xaa	

70	75	80	
GTG GCA CTG TCA GCC CAG CCC TCC CTA CCG GCG AGA GTC CAG AGT			382
Val Ala Leu Ser Ala Gln Pro Ser Leu Pro Ala Arg Val Gln Ser			
85	90	95	

## (2) INFORMATION FOR SEQ ID NO: 225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..139)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 135..272  
id HSB82C022  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 10..108
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8  
seq FTSASLLLPMTG/MP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

ATTATTTAT ATG ATT AAC CCC TCA GTC CCT AGC AAG TCA AAT TCC CAT CCG	51
Met Ile Asn Pro Ser Val Pro Ser Lys Ser Asn Ser His Pro	
-30 -25 -20	
TTT TTA TCT ACA GTA ATG TTC ACC TCT GCA TCA CTG CTG CTT CCC ATG	99
Phe Leu Ser Thr Val Met Phe Thr Ser Ala Ser Leu Leu Leu Pro Met	
-15 -10 -5	
TCT ACA GGC ATG CCA ACT CAA AAC TGT TTT ACC CCA AAG	138
Ser Thr Gly Met Pro Thr Gln Asn Cys Phe Thr Pro Lys	
1 5 10	

## (2) INFORMATION FOR SEQ ID NO: 226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 138..186

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91  
region 14..62  
id AA111755  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 83..286

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.7  
seq IACLAWWIGGSG/XN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

AAAGACTTTG CGAASGCTGC GCTCGCGCCC GGATCCCTCA GCGGCTGCA GGCTTCASCC    60
TGCCTGGTT GGTGAAACAG AG ATG TCA GAA AAG GAG AVC AAC TTC CCG CCA    112
      Met Ser Glu Lys Glu Xaa Asn Phe Pro Pro
      -65                                -60

CTG CCC AAG TTC ATC CCT GTG AAG CCC TGC TTC TAC CAG AAC TTC TCC    160
Leu Pro Lys Phe Ile Pro Val Lys Pro Cys Phe Tyr Gln Asn Phe Ser
      -55                                -50                                -45

GAC GAG ATC CCA GTG GAG CAC CAG GTC CTG GTG AAG AGG ATC TAC CGG    208
Asp Glu Ile Pro Val Glu His Gln Val Leu Val Lys Arg Ile Tyr Arg
      -40                                -35                                -30

CTG TGG ATG TTT TAC TGC GCC ACC CTC GGC GTC AAC CTC ATT GCC TGC    256
Leu Trp Met Phe Tyr Cys Ala Thr Leu Gly Val Asn Leu Ile Ala Cys
      -25                                -20                                -15

CTG GCC TGG TGG ATC GGC GGA GGC TCG GGG NNB AAC TTC GGC CTG GCC    304
Leu Ala Trp Trp Ile Gly Gly Gly Ser Gly Xaa Asn Phe Gly Leu Ala
      -10                                -5                                1                                5

TTC GTG TGG CTG CTC CTG TTC ACG CCT TGC GGC TAC GTG TCC TGG TTC    352
Phe Val Trp Leu Leu Leu Phe Thr Pro Cys Gly Tyr Val Cys Trp Phe
      10                                15                                20

GGG CCT GTC TAC AAG GCC TTC CGA GCC GAC AGC TCC TTT AAT TTC ATG    400
Arg Pro Val Tyr Lys Ala Phe Arg Ala Asp Ser Ser Phe Asn Phe Met
      25                                30                                35

GGG CTG
Ala Leu
      40

```

406

## (2) INFORMATION FOR SEQ ID NO: 227:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(68..131)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 392..455  
id W22335  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 288..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 9..68  
id H70453  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 159..227
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq ILRLYFFLQLAHS/GY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```

ACGAAATGGT ATTGACATCT TGSTTGAAC ACCTGGTCGT ATCAAAGACC ATCTGCAGAG   60
TGGCCGATTG GATCTTTCTA AACTGCGACA TGTTGTGCTT GATGAAGTGG ATCAGATGTT  120
AGATTTAGGT CTCGCTGAAC AAGTTGAAGA TATTATTC ATG AAT CCT ACA AAA CTG   176
                               Met Asn Pro Thr Lys Leu
                               -20

ATT CTG AAG ACA ATC CTC AGA CTT TAC TTT TTT CTG CAA CTT GCC CAC   224
Ile Leu Lys Thr Ile Leu Arg Leu Tyr Phe Phe Leu Gln Leu Ala His
   -13                               -10                               -5

AGT GGG TAT ACA AAG TTG CAA AAA AAA TAC ATG AAA TCC ACA TAT GAA   272
Ser Gly Tyr Thr Lys Leu Gln Lys Lys Tyr Met Lys Ser Arg Tyr Glu
    1                               5                               10                               15

CAG GTT GAG CTT GTT GGR AAA ATG WCT CAA AAG GCT GCA AAT ACT GTG   320

```

Gln Val Asp Leu Val Gly Lys Met Xaa Gln Lys Ala Ala Thr Thr Val  
20 25 30  
GRA CAT TTG GCC ATC CAG TGT CAT TGG 347  
Xaa His Leu Ala Ile Gln Cys His Trp  
35 40

## (2) INFORMATION FOR SEQ ID NO: 228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..70
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..59  
id AA013305  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 197..250
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 189..242  
id AA013305  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 250..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 243..290  
id AA013305  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..199
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 236..299  
id R48472  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 37..101  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 135..199  
 id R48472  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 38..106  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.7  
 seq SXXCFVSVPPASA/IP

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```

AACCCGGGAC CGAGCTGGGG TCTTGAGGA AGAGAGG ATG GCG TCG TCG ACC CCT      55
                               Met Ala Ser Ser Ser Pro
                               -20

GAC TCC CCA TGT TCC TGS NAC TGC TTT GTC TCC GTG CCC CCG GGC TCA      103
Asp Ser Pro Cys Ser Xaa Xaa Cys Phe Val Ser Val Pro Pro Ala Ser
      -15                      -10                      -5

GCC ATC CCG GST GTG AKC TTK GCC NNH AAC TCG GAC SGA CCC CCG GAC      151
Ala Ile Pro Xaa Val Xaa Xaa Ala Xaa Asn Ser Asp Xaa Pro Arg Asp
      1                      5                      10                      15

GAG GTG CAG GAG GTG GTG TTT GTC CCC GCA GGC ACT CAC ACT CCT GGG      199
Glu Val Gln Glu Val Val Phe Val Pro Ala Gly Thr His Thr Pro Gly
      20                      25                      30

AGC CGG CTC CAG TGC ACC TAC ATT GAA GTG GAA CAG GTG TCG AAG ACG      247
Ser Arg Leu Gln Cys Thr Tyr Ile Glu Val Glu Gln Val Ser Lys Thr
      35                      40                      45

CAC GGT GTG ATT CTG AGC CGT CCT TCT TGG CTA TGG GGG GCT GAG ATG      295
His Ala Val Ile Leu Ser Arg Pro Ser Trp Leu Trp Gly Ala Glu Met
      50                      55                      60

GGC GMV AGG AGC ATG GTG TCT GCA TTG GCA ACG AGG CTG TGT GGA CGA      343
Gly Xaa Thr Ser Met Val Ser Ala Leu Ala Thr Arg Leu Cys Gly Arg
      65                      70                      75

AGG AGC CAG TTG GGG AGG GCN GKN GCC CTS CTG GGC ATG GAC CTA CTC      391
Arg Ser Gln Leu Gly Arg Ala Xaa Ala Leu Leu Gly Met Asp Leu Leu
      80                      85                      90                      95

AGG TGC AGA CCC TGC                                          406
Arg Cys Arg Pro Cys
      100
  
```

## (2) INFORMATION FOR SEQ ID NO: 229:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 128..197

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 158..227  
id AA249540  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 241..309

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92  
region 267..335  
id AA249540  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 164..240

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 58..134  
id N46699  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 128..161

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 23..56  
id N46699  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(224..309)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 104..189  
id W39777  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 233..309

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 13..89  
id AA036848  
est



## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 233..309  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 13..89  
id AA133513  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 171..287  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq XLIAXLEPPGAMA/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```
CATTATTCCT TTTCCATCGG AAGTGGCGCT CGTGCATTCA ACTTGTTCCC GTCATGGAA    60
CCCCTCTTTA AAAAGACGCA GGGCACCTGT GAGCGCAGGA GCGAGCCTAA GGCCACCCAG    120
CGGCAGCGCC CGTGTCTTGG GCACTCAGCG TGCTGGGCAG AGCAGGTGCG ATG GSC      176
                                   Met Xaa
CCA GTC CTA GCA GCC CTC GCC CAT GTC CTG TGC CCT TAC ATG GCT CCC      224
Pro Val Leu Ala Ala Leu Ala His Val Leu Cys Pro Tyr Met Ala Pro
   -35                               -30                               -25
GGA CTG TGC AGG GAG CCG ATA CGT TTK CTG ATA GCA VTA CTG GAA CCA      272
Gly Leu Cys Arg Glu Pro Ile Arg Xaa Leu Ile Ala Xaa Leu Glu Pro
   -20                               -15                               -10
CCG GGT GCG ATG GCA GTC AGG AGA CTG CCC AGT GCC                        308
Pro Gly Ala Met Ala Val Arg Arg Leu Pro Ser Ala
   -5                               1                               5
```

## (2) INFORMATION FOR SEQ ID NO: 230:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..327  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..309

id C16848  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 75..104  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 303..332  
id R40385  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 73..207  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq PMLGLAAFRWIWS/RE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```

AAAAGCGGAC CCGCGGACGG TGGCGTTAAG GGAACGCTGA GGTCCCGCGC TCCCCGACCG      60
AGGTATATCT CC ATG AAT AAC CTA AAT GAT CCC CCA AAT TGG AAT ATC CGG      111
      Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile Arg
      -45                      -40                      -35

CCT AAT TCC AGG GCG GAT GGT GGT GAT GGA AGC AGG TGG AAT TAT GCC      159
Pro Asn Ser Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr Ala
      -30                      -25                      -20

CTG TTG GTT CCA ATG CTG GGA TTG GCT GCT TTT CGT TGG ATT TGG TCT      207
Leu Leu Val Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp Ser
      -15                      -10                      -5

AGG GAG TCC CAG AAA GAA GTA GAA AAA GAG AGA GAA GCC TAC CGT CGG      255
Arg Glu Ser Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg
      1                      5                      10                      15

AGA ACT GCT GCT TTT CAA CAG GAT CTG GAA GCC AAG TAC CAC GCC ATG      303
Arg Thr Ala Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala Met
      20                      25                      30

ATC TCA GAM AAT CGG CGT GCT GTC      327
Ile Ser Xaa Asn Arg Arg Ala Val
      35                      40

```

## (2) INFORMATION FOR SEQ ID NO: 231:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (11) MOLECULE TYPE: CDNA

## (12) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(3..297)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..295  
id W57719  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(37..300)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 10..273  
id H04979  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(7..41)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 270..304  
id H04979  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(37..295)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 7..265  
id H10390  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..41)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 262..301  
id H10390  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(142..295)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..154  
id W42765  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..141)  
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 156..295  
id W42765  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(55..238)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 71..254  
id R39116  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(255..297)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 10..52  
id R39116  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 295..351  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.6  
seq AALCSLFFFLSLQ/EI

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```

ACGTTAGGGG GCCAGGGAGA TGTGACTGAG GCTGGCTTTC CACGTGAATC AGACGGGGTC   60
GGTGGAGGGT TTGGTGCTAC AGCCAGTCAG AAGATTTGCA AATGCGAACA CATTCCTGTG   120
TGAGGCACGT TACCCTTTGT CAGTTATTGT GAATATGTGT ATTTTAAGCA ATAAGATTCA   180
GCTGGTCAGA CTTTTCTGGG CAGTCTCAGT GACGCATTTC CTGTGCTGTG ATTGTTCTGA   240
AGACAGAGTG GCTCTAACCA CTGTGAGAAG CCCAAATAAA AATTGATCCC AAAA  ATG   297
                                     Met
CTA CTG CTC TTT CTT GCT GCA CTT TGT TCC CTC TTC TTC TTC CTC AGT   345
Leu Leu Leu Phe Leu Ala Ala Leu Cys Ser Leu Phe Phe Phe Leu Ser
      -15                      -10                      -5

CTT CAG GAA ATT GCA CCT CAA GAT CCC AAA CCA GGG   381
Leu Gln Glu Ile Ala Pro Gln Asp Pro Lys Pro Gly
      1                      5                      10

```

## (2) INFORMATION FOR SEQ ID NO: 232:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 17..175

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91  
region 1..159  
id W51023  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 42..173

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..132  
id T61976  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 2..142

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.5  
seq IIVCLFAFLVAHC/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```
T ATG TTA TTC CTT GGC AAG GTG CTG ATA GTC TGC AGC ACA GGT TTA GCT   49
Met Leu Phe Leu Gly Lys Val Leu Ile Val Cys Ser Thr Gly Leu Ala
    -45                -40                -35

GGG ATT ATG CTG CTC AAC TAC CAG CAG GAC TAC ACA GTA TGG GTG CTG   97
Gly Ile Met Leu Leu Asn Tyr Gln Gln Asp Tyr Thr Val Trp Val Leu
    -30                -25                -20

GGT CTG ATC ATC GTC TGC CTC TTT GCT TTC CTA GTC GCT CAT TGC TTC  145
Pro Leu Ile Ile Val Cys Leu Phe Ala Phe Leu Val Ala His Cys Phe
    -15                -10                -5                1

CTG TCT ATT TAT GAA ATG GTA GTC GAT GCG AGG   178
Leu Ser Ile Tyr Glu Met Val Val Asp Ala Arg
    5                10
```

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..321)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 59..378  
id AA045815  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..150  
id R18658  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 240..321
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 147..228  
id R18658  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..321
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..227  
id R14615  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..200)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 3..201  
id N95174  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(36..197)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 8..169  
id N93742  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..44)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 166..208  
id N93742  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 191..304  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq LLLLVHSEFWFTVC/TP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```
AAGACTCATA GAGATTAAAT GATCACTATG GTCCTTCTTC TGTTAAATGG AGCCAAAGAC    60
GCCTATGTTG TTCTGAAGTC TTGTAATGTT TAACTTCIGA GAACTTAGAT TAGTGGTGTG   120
ATGATAGAGT CTGTATAACG CATTGAAAAG GGTATCAGGC TTAGTTATTT ATCCAATAAA   180
TATTTATTGT ATG CAG GGT ATT CCT ATT TTA ACT CCT GTG ACA ACA CAA       229
      Met Gln Gly Ile Pro Ile Leu Thr Pro Val Thr Thr Gln
                        -35                               -30

AGC ATA GCG ATT TCC ATA GTT CTA ACT GTT CAG GGT CTG CTC CTC CTG       277
Ser Ile Ala Ile Ser Ile Val Leu Thr Val Gln Gly Leu Leu Leu Leu
-25                -20                -15                -10

GTA CAC TCT TTT TGG TTC ACT GTA TGT ACT CCT GTT GTC TTT             319
Val His Ser Phe Trp Phe Thr Val Cys Thr Pro Val Val Phe
      -5                        1                        5
```

## (2) INFORMATION FOR SEQ ID NO: 234:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(131..360)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 45..274  
id M78402  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(57..234)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 10..187  
id H04786  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(7..43)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 201..237  
id H04786  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(57..234)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 10..187  
id H17078  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(7..43)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 201..237  
id H17078  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(57..217)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..161  
id HSC0UC022  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..43)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 175..217  
id HSC0UC022  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 199..279  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq LFCVLLSLRPHTS/GT



(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

ACAAGATTTT CCAACCTTGC TGGCTACTTT AGTTTGGGAC CTGTTTTTTT TCTCATTTGA    60
TTTTTCCTTGT GCAGAAAATA GTTTCAGCA CATGGATTGA TCTCAGAGAC AATGAGGCTC    120
AGTTTGTGGAT AGTCTGTTTT CTCTGAGCAT GTTGCCCAAC TAGTATGCTC AAATTATTGA    180
GTGGATCATC TCTTGGAA ATG CAG AAC TTC TGC CAC CAC TGG GGT ATT TGC    231
                Met Gln Asn Phe Cys His His Leu Ala Ile Cys
                -25                                -20

ACA GTC ATC TTG TTC TGT GTC CTT TTA TCT CTC AGA CCA CAC ACA TCT    279
Thr Val Ile Leu Phe Cys Val Leu Leu Ser Leu Arg Pro His Thr Ser
   -15                -10                -5

GCA ACG CTG TGG GCA TCT TCT GCC CAT GGG CTC CAT TTG GCA CCT GCT    327
Gly Thr Leu Trp Ala Ser Ser Ala His Gly Leu His Leu Ala Pro Ala
   1                5                10                15

GAG CCA CAG TTG TCC TGC TGG ATG TGC TGT GCA    360
Glu Pro Gln Leu Ser Cys Trp Met Cys Cys Ala
                20                25

```

(2) INFORMATION FOR SEQ ID NO: 235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 35..326  
id H97426  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 92..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 14..238  
id W44834  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 127..177  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 4..54  
                           id R57989  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..211  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 62..91  
                           id R57989  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(287..316)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 385..414  
                           id N93806  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 34..225  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.3  
                           seq VLMRLVASAYSIA/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

AAGTTTCCCG CATGCTCAGT AGCTGAGGTA GGG ATG CCA TCC TTC TCA AAA GAC	54
Met Pro Ser Phe Ser Lys Asp	
-60	
TTA TTG ACA GTG CCA AAG CTC GGT ACT GGA CAC VMC GRR GGR MCT GGG	102
Leu Leu Thr Val Pro Lys Leu Gly Thr Gly His Xaa Xaa Gly Xaa Gly	
-55 -50 -45	
TCC TAC GAT RAC GCG CTT KTG CTC CTC CTG AAG TGT CTT TGG TCC AAC	150
Ser Tyr Asp Xaa Ala Leu Xaa Leu Leu Lys Cys Leu Trp Ser Asn	
-40 -35 -30	
GTT GTT CCA GAG TGT ACC ATG GCT TCC AGT AAC ACT GTG TTG ATG CGG	198
Val Val Pro Glu Cys Thr Met Ala Ser Ser Asn Thr Val Leu Met Arg	
-25 -20 -15 -10	
TTG GTA GCC TCC GCA TAT TCT ATT GCT CAA AAG GCA GGA ATG ATA GTC	246
Leu Val Ala Ser Ala Tyr Ser Ile Ala Gln Lys Ala Gly Met Ile Val	
-5 1 5	
AGA CGT GTT ATT GCT GAA GGA GAC CTG GGT ATT GTG GAG AAG ACC TGT	294
Arg Arg Val Ile Ala Glu Gly Asp Leu Gly Ile Val Glu Lys Thr Cys	
10 15 20	
GCA ACA GAC CTG CAG ACC AAA GCT GAC CGA TTG GCA CAG ATG AGC ATA	342
Ala Thr Asp Leu Gln Thr Lys Ala Asp Arg Leu Ala Gln Met Ser Ile	

25	30	35	
TGT TCT TCA TTG GYM BGG AAA TTC CCC AAA CTC RNR ATT ATA GGG GAA			390
Cys Ser Ser Leu Xaa Xaa Lys Phe Pro Lys Leu Xaa Ile Ile Gly Glu			
40	45	50	55
GAG GAT CTG CTT TGT GAG GAA GTG GAT CAA GAG CTG ATT GAA GAC AGK			438
Glu Asp Leu Pro Ser Glu Glu Val Asp Gln Glu Leu Ile Glu Asp Xaa			
60	65	70	

## (2) INFORMATION FOR SEQ ID NO: 236:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..121  
id W04921  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 114..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 121..227  
id W04921  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 221..310
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 227..316  
id W04921  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(114..213)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 260..353  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(32..113)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 359..440  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(261..311)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 164..214  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(213..259)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 215..261  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 114..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 59..139  
id W70167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 238..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 183..256  
id W70167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..59  
id W70167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..236
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 139..182

id W70167  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 221..311  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 165..255  
id W37690  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 114..187  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 58..131  
id W37690  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 56..113  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..58  
id W37690  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 185..220  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 130..165  
id W37690  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 227..289  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.2  
seq LEMLKAFASHIXA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```
ATGCGACGCTT CCTTGGCTCG GCTTGGTCTG CGGCCTGTCA AACAGGTTTC GGTTCAGTTC 60
TGTCCCTTCG AGAAAAACGT GGAATCGACG AGGACCTTCV TSCAGACGGT GAGGCMGTGA 120
GAAGGTCCGC TCCACTAATC TCAACTGCTC AGTGATTGCG GACGTGASGC ATGACGGCTC 180
CGAGCCCTGC GTGGACGTGC TGTTCCGAGA CGGGCATCGC CIGATT ATG CGC GGC 235
Met Arg Gly
-20
GCT CAT CTC ACC GCT CTG GAA ATG CTC ANM GCC TTC GCC TCC CAC ATM 283
Ala His Leu Thr Ala Leu Glu Met Leu Xaa Ala Phe Ala Ser His Ile
```

-15

-10

-5

HGG GCC AGG GAC GCG GCG GGC AGC GGG  
Xaa Ala Arg Asp Ala Ala Gly Ser Gly  
1 5

310

## (2) INFORMATION FOR SEQ ID NO: 237:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 321..431
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 186..296  
id AA043558  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 218..299
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 83..164  
id AA043558  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 39..96  
id AA043558  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..299
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 57..225  
id N50523  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 321..431

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 247..357  
id N50523  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(45..115)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..71  
id N50523  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(321..431)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 289..399  
id AA115605  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(217..318)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 403..504  
id AA115605  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(166..231)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 491..556  
id AA115605  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 172..318  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 36..182  
id AA115129  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 321..431  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 186..296  
id AA115129  
est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 174..318  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 41..185  
                           id AA035548  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 325..431  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 194..300  
                           id AA035548  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 7..423  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.2  
                           seq FGLLHQLSQCVTS/LE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

ACAAGG ATG GAA GTG GGC TTA CCG GCC ATT ACC CTC TTT CTC ACC AGC	48
Met Glu Val Gly Leu Pro Ala Ile Thr Leu Phe Leu Thr Ser	
-135 -130	
GCC AGC AGC CCT GTG GTG GCG ACG ACG ATG GAC CAG GAG CCA GTG GGC	96
Ala Ser Ser Pro Val Val Ala Thr Thr Met Asp Gln Glu Pro Val Gly	
-125 -120 -115 -110	
GGT GTG GAA CGA GGA GAA GCC GTC GCA GCC TCG CGA RCT GCG GCC GCC	144
Gly Val Glu Arg Gly Glu Ala Val Ala Ala Ser Gly Xaa Ala Ala Ala	
-105 -100 -95	
GCG GCA TTC GGG GAA TCT GCA GGG CAG ATG AGT AAC GAA AGA GGC TTT	192
Ala Ala Phe Gly Glu Ser Ala Gly Gln Met Ser Asn Glu Arg Gly Phe	
-90 -85 -80	
GAA AAT GTA GAA CTG GGA GTC ATA GGA AAA AAG AAG AAA GTC CCA AGG	240
Glu Asn Val Glu Leu Gly Val Ile Gly Lys Lys Lys Lys Val Pro Arg	
-75 -70 -65	
AGA GTC ATC CAC TTT GTT AGT GGT GAA ACA ATG GAA GAA TAT AGC ACA	288
Arg Val Ile His Phe Val Ser Gly Glu Thr Met Glu Glu Tyr Ser Thr	
-60 -55 -50	
GAT GAA GAC GAA GTT GAT GGC CTG GAG AAG NNG ATG TTT TGC CTA CTC	336
Asp Glu Asp Xaa Val Asp Gly Leu Glu Lys Xaa Met Phe Cys Leu Leu	
-45 -40 -35 -30	
TTG ATC CGR CAA AAC TTA CCT GGG GTC CCT ACT TAT GGT TTT ACA TGC	384
Leu Ile Arg Gln Asn Leu Pro Gly Val Pro Thr Tyr Gly Phe Thr Cys	
-25 -20 -15	
TTG GGG CTG CTA CAT CAA CTC TCT CAG TGT GTG ACT TCC TTG GAG	429
Phe Gly Leu Leu His Gln Leu Ser Gln Cys Val Thr Ser Leu Glu	



-10

-5

1

## (2) INFORMATION FOR SEQ ID NO: 233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 31..251  
id T34679  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 104..250  
id N34677  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..170
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 21..98  
id N34677  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 190..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 203..335  
id N32531  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 202..334  
id N36824

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..170
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 28..96  
id N36824  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 175..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 100..237  
id H97539  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 151..279
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq SAATLASLGGTSS/RR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

```

AACTCTCGTG CCAAGCATGT CTCTCCAAAT GGCTGCTCTC TGGCGTTCTT CACACTCCCC   60
CTGAAGTTCA TCTAAGATCT TCATTCTTCA WAGGCGGAAG CCCGGCTCGC TGCAAAACGG   120
GGGGCCCCGG CGGAGGCTCG CGAGATCCGC ATG AAG GAG CTG GAG CGG CAG CAG   174
                               Met Lys Glu Leu Glu Arg Gln Gln
                               -40

AAG GAG GTA GAA GAG AGA CCA GAA AAA GAT TTT ACT GAG AAG GGG TCT   222
Lys Glu Val Glu Glu Arg Pro Glu Lys Asp Phe Thr Glu Lys Gly Ser
-35                -30                -25                -20

CGT AAC ATG CCG GGC CTG TCT GCA GCC ACG CTG GCC TCT CTG GGT GGG   270
Arg Asn Met Pro Gly Leu Ser Ala Ala Thr Leu Ala Ser Leu Gly Gly
          -15                -10                -5

ACT TCC TCT CGG AGA GGC AGC GGA GAC ACC TCC ATC TCC ATC GAC CCC   318
Thr Ser Ser Arg Arg Gly Ser Gly Asp Thr Ser Ile Ser Ile Asp Pro
          1                5                10

GAG
Glu
                                           321

```

## (2) INFORMATION FOR SEQ ID NO: 239:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 270..403

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92  
region 199..332  
id AAL25491  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 70..135

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 1..66  
id AAL25491  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(27..135)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 89..197  
id HSB72F052  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(135..223)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 2..90  
id HSB72F052  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 126..188

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.1  
seq VLVILCIVTVCVT/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```
ACCGGAGAAA AAATGGTTCA TGGAGCCTGC CGTAT7TGTT TGCCTGGGTG GAATTTTACC   60
TTTTGGTTCA ATCTTTAT7G AAATGTATTT CATCTTCACG TCTTTCTGGG CATATAAGAT  120
CTATT ATG TCT ATG GGC TTC ATG ATG CTG GTG CTG GTT ATC CTG TGC ATT  170
Met Ser Met Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile
-20 -15 -10
```

GTG ACT GTC TGT GTG ACT ATT GTG TGC ACA TAT TTT CTA CTA AAT GCA	218
Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala	
-5 1 5 10	
GAA GAT TAC AGG TGG CAA TGG ACA AGT TTT CTC TCT GGT GCA TCA ACT	266
Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr	
15 20 25	
GCA ATC TAT GTT TAC ATG TAT TCC TTT TAC TAC TAT TTT TTC AAA ACA	314
Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr	
30 35 40	
AAG ATG TAT GGC TTA TTT CAA ACA TCA TTT TAC TTT GGA TAT ATG GCG	362
Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala	
45 50 55	
GTA TTT AGC ACA GCC TTG GGG ATA ATG TGT GGA GCG ATT	401
Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile	
60 65 70	

## (2) INFORMATION FOR SEQ ID NO: 240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..397
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 131..375  
id W56159  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..121  
id W56159  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..467
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 303..617

id HS278368  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 214..293  
id HS278368  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 153..374  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 80..301  
id AA026570  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 70..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..70  
id AA026570  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 372..405  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 300..333  
id AA026570  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 155..467  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 83..395  
id AA109961  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 88..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 20..71  
id AA109961  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 153..363  
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 274..484  
id AA046907  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 185..264  
id AA046907  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 128..337  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6  
seq LLEPLTLVRSFWS/DM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```

AACGCTTGCG ATGGTTGAAT TCCCCTCCTC ACGCCAGCCT AGGAGAAGAA GTTCGTAGTC      60
CCAGAGGAAG AGGAGTTGTA CGCATGTCAG AGAGCTTGCA GGCTGTTTTT AATTTGTCAG    120
TTTGTGG ATG ATG GAA TTG GRM CTW AAA AKC GRA ACT AAA KKG GAA TGK      169
      Met Met Glu Leu Xaa Leu Lys Xaa Xaa Thr Lys Xaa Glu Xaa
      -70                      -65                      -60
GAA TCT GCA TGT ACA GAA GCA TAT TCC CAA TCT GAT GAG CAA TAT GCT      217
Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
      -55                      -50                      -45
TGC CAT CTT GGT TGC CAG AAT CAG CTG CCA TTC GCT GAA CTG AGA CAA      265
Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
      -40                      -35                      -30                      -25
GAA CAA CTT ATG TCC CTG ATG CCA AAA ATG CAC CTA CTC TTT CCT CTA      313
Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
      -20                      -15                      -10
ACT CTG GTG AGG TCA TTC TGG AGT GAC ATG ATG GAC TCC GCA CAG AGC      361
Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
      -5                      1                      5
TTC AKA ACC TCT TCA TGG ACT TTT TAT CTT CAA GCC GAT GMC GGM MAA      409
Phe Xaa Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Xaa Gly Xaa
      10                      15                      20
ATA GTT ATA TKC CAG TCT AAG CCA GAA ATC CAG TAC GCA CCA CAT TTG      457
Ile Val Ile Xaa Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu
      25                      30                      35                      40
GAG CAG GAG
Glu Gln Glu

```

## (2) INFORMATION FOR SEQ ID NO: 241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..81
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 62..125  
id AA092155  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 68..131  
id AA128307  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 68..131  
id N99068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 68..131  
id AA039944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 68..131  
id AA128099  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

- (B) LOCATION: 1..72
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq GLILLFASHLINQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

ATG GTT TCC AAT GGT TCR GAG ACT TCC TGC CTA GGC CTC ATC CTC CTC 48  
Met Val Ser Asn Ala Ser Gln Thr Ser Cys Leu Gly Leu Ile Leu Leu  
-20 -15 -10

TTT GCC AGT CAC CTG ATT AAC CAA TTC TCC AGC 81  
Phe Ala Ser His Leu Ile Asn Gln Phe Ser Ser  
-5 1

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..274  
id H18735  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 116..275  
id T80360  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 51..115  
id T80360  
est

(ix) FEATURE:

- (A) NAME/KEY: other



(B) LOCATION: 29..69  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..41  
id T30360  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 66..302  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..237  
id AA137006  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 301..336  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 412..447  
id AA137006  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 65..302  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 2..239  
id HSC2CA081  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 64..224  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..161  
id T36290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 223..302  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 161..240  
id T36290  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 2..220  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6  
seq LIVFISVCTALLA/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```

A ATG CCC CGG AAG CGG AAG TGC GAT CTT CGG GCT GTC AGA GTT GGT CTG   49
  Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
    -70                      -65                      -60

TTA CTC GGT GGT GGC GGA GTC TAC GGA AGC CGT TTT CGC TTC ACT TTT   97
Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
  -55                      -50                      -45

CCT GGC TGT AGA GCG CTT TCC CCC TGG CGG GTG AGA VTG CAG AGA CGA  145
Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
  -40                      -35                      -30

AGC TGC GAG ATG AGC ACT ATG TTC GCG GAC ACT CTC CTC ATC GTT TTT  193
Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
  -25                      -20                      -15                      -10

ATC TCT GTG TGC ACG GCT CTG CTC GCA GAG GGC ATA ACC TGG STC CTG  241
Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
    -5                      1                      5

GTT TAC AGG ACA GAC AAG TAC AAG AGA CTG AAG GCA GAA GTG GAA AAA  289
Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
    10                      15                      20

CAG AGT AAA AAA TAT TTG ATG GTA GAG TGG TGG CAA ASC TTC CTT TTT  337
Gln Ser Lys Lys Tyr Leu Met Val Glu Trp Trp Gln Xaa Phe Leu Phe
    25                      30                      35

TAC CCC TCT TTC TTA SAT CCA AAG RCT GTC TCA TCG   373
Tyr Pro Ser Phe Leu Xaa Pro Lys Xaa Val Ser Ser
    40                      45                      50

```

## (2) INFORMATION FOR SEQ ID NO: 243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 159..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 121..269  
id W31320  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..121

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..85  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 320..380  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 282..342  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 114..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 77..128  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 400..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 364..407  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 154..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..155  
id T27259  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 320..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 168..291  
id T27259  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 192..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 108..223  
id AA157646  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 64..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..32  
id AA157646  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 320..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 123..246  
id AA182962  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 198..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..110  
id AA182962  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 243..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 189..253  
id T71690  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 181..235  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 125..179  
id T71690  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 114..164  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 58..108  
id T71690  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 130..198  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq LGAAALALLLANT/DV

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```

CCCCGCCCT GGGACCCCTCC GGGCCGGGCG GTTGTGGCCCC TTAGCGCCCG GCGCTCGGGG 60
CGGTAAAAGG CCGGCAGAAG GGAGGCACCT GAGAAATGTC TTCTCTCCAG GACCCAAAGT 120
TTCTTCACC ATG GGG ATG TGG TCC ATT GGT GCA GGA GCC CTG GGG GCT GCT 171
      Met Gly Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala
            -20                -15                -10

GCC TTG GCA TTG CTG CTT GCC AAC ACA GAC GTG TTT CTG TCC AAG CCC 219
Ala Leu Ala Leu Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro
            -5                1                5

CAG AAA GCG GCC CTG GAG TAC CTG GAG GAT ATA GAC CTG AAA ACA CTG 267
Gln Lys Ala Ala Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu
            10                15                20

GAG AAG GAA CCA AGG ACT TTC AAA GCA AAG GAG CTA TGG GAA AAA AAT 315
Glu Lys Glu Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn
            25                30                35

GGA GCT GTG ATT ATG GCC GTG CGG AGG CCA GGC TGT TTC CTC TST CGA 363
Gly Ala Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg
            40                45                50                55

GAG GAA GCT GCG GAT CTG TCC TCC CTG AAA AGC ATG TTG GAC CAG CTG 411
Glu Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu
            60                65                70

GGC GTC CCC CTC TAT GCA GTG GTA AAG GAG CAA CGG 447
Gly Val Pro Leu Tyr Ala Val Val Lys Glu Gln Arg
            75                80

```

## (2) INFORMATION FOR SEQ ID NO: 244:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 13..394  
id C17481  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 379..424  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 390..435  
id C17481  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 65..255  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 72..262  
id T46941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 1..67  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 6..72  
id T46941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(149..271)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 1..123  
id R75331  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 257..430  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 42..215  
id W95977  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 278..430  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 5..157  
id R57521  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 255..347  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq LPLLLVANAGTAA/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

```

ATGAAAATGG GTGTGCTTAT TTCCACGAAG AGGAAACAGA AGGACTTGCA AAGATATGTA    60
GGCTTGCCAT TCATTCTCGA TAIGAAGACT TCGTAGTGGA TGGCTTCAAT GTGTTATATA   120
ACAAGAAGCC TGTCATATAT CTTAGTGCTG CTGCTAGACC TGGCCTGGGC CAATACCTTT   180
GTAATCAGCT CGGCTTGCCC TTCCCTTGCT TGTGCCGTGT ACCCTGTAAC ACTGTGTTTG   240

GATCCCAGCA TCAG ATG GAT GTT GCC TTC CTG GAG ADA CTG ATT AAA GAT    290
          Met Asp Val Ala Phe Leu Glu Xaa Leu Ile Lys Asp
          -30                      -25                      -20

GAT ATA GAG CGA GGA AGA CTG CCG CTG TTG CTT GTC GCA AAT GCA GGA    338
Asp Ile Glu Arg Gly Arg Leu Pro Leu Leu Leu Val Ala Asn Ala Gly
          -15                      -10                      -5

ACG GCA GCA GTA GGA CAC ACA GAC AAG ATT GGG AGA TTG AAA GAA CTC    386
Thr Ala Ala Val Gly His Thr Asp Lys Ile Gly Arg Leu Lys Glu Leu
          1                      5                      10

TGT GAG CAG TAT GGC ATA TGG CTT CAT GTG GAG GGT GTG AAT          428
Cys Glu Gln Tyr Gly Ile Trp Leu His Val Glu Gly Val Asn
    15                      20                      25

```

## (2) INFORMATION FOR SEQ ID NO: 245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 3..232  
id HSC1WH101  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 41..169  
id R12437  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 63..104  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..42  
id R12437  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 63..230  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..168  
id R13448  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 165..212  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 36..83  
id T69236  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 180..227  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.8  
seq LFNLLWLALACSP/VW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

```

GTTTGTGGCC GTCCGGCCTC CCTGACATGC AGATTTCAC CCAGAAGACA GAGAAGGAGC   60
CAGTGGTCAT GGAATGGGCT GGGGTCAAAG ACTGGGTGCC TGGGAGCTGA GGCAGCCACC  120
GTTTCAGCCT GGCCAGCCCT CTGGACCCCG AGGTTGGACC CTACTGTGAC ACACCTACC   179
ATG CGG ACA CTC TTC AAC CTC CTC TGG CTT GCC CTG GCC TGC AGC CCT   227
Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
   -15                   -10                   -5

GTT TGG                                     233
Val Trp
1
```

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 178..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 118..271  
id R60406  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 178..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 57..195  
id N78477  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 214..312
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq FICLQWALPHSEA/GD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

AAAGGCAGGA CTGACGCAGA ATGACAACGG CAACACGACA AGAAGTCCTT GGCCTCTACC   60
GCAGCATTTT CAGGCTTGCG AGGAAATGGC AGGCGACATC AGGGCAGATG GAAGACACCA   120
TCAAAGAAAA ACAGTACATA CTAAATGAAG CCAGAACGCT GTTCGGGAAA AACAAAAATC   180
TCACGGACAC AGACCTAATT AAACAGTGTA TAG ATG AAT GCA CAG CCA GGA TTG   234
                               Met Asn Ala Gln Pro Gly Leu
                               -30

AWA TTG GAC TGC ATT ACA AGA TTC CTT ACC CAN GGC CAA TTC ATC TGC   282
Xaa Leu Asp Cys Ile Thr Arg Phe Leu Thr Xaa Gly Gln Phe Ile Cys
-25                               -20                               -15

CTC CAA TGG GCC TTA CCC CAC TCC GAG GCC GGG GAC TTC GAA GCC AAG   330
Leu Gln Trp Ala Leu Pro His Ser Glu Ala Gly Asp Phe Glu Ala Lys
-10                               -5                               1                               5

```

## (2) INFORMATION FOR SEQ ID NO: 247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(230..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 32..154  
id W60134  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(78..189)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 195..306  
id W60134  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..87)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 298..376  
id W60134  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(176..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 57..233  
id H64097  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(57..189)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 219..351  
id H64097  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(34..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 57..325  
id W00624  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(1..70)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 337..406  
id W00624  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..168)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 156..323  
id W67127  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(167..323)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..158  
id W67127  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(64..352)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 58..346  
id H10776  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(23..64)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 347..388  
id H10776  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 120..326  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq LCRLCLVRLFC/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```
ATTGGGGAG GGSCACTGTC TCTTTTCTCT CTCATTTTAA AATGAAGTG TTGTTGCCTT    60
TGTATGTGGT TCAACCATCC AGCTCCACG TGGCTAAACT TTGCTCCAG TGGTCAAAG    119
ATG GCA AAA GAG TGG GGT TGG CAG GAG ATG GAA AAC GGA GGT GCC GCC    167
Met Gly Lys Glu Trp Gly Trp Gln Glu Met Glu Asn Gly Gly Ala Ala
      -65                -60                -55
```

CCA GCA TGG GGG GCA GGT GGG GCA GTC CAC CCT GCC CCT CCC CCT GTG	215
Pro Ala Trp Gly Ala Gly Pro Pro Val His Pro Ala Pro Pro Pro Val	
-50 -45 -40	
GAG AAG ACG CTT AGT TGG GGG TGT GGG TTT GGG CTC CAT TCT GGA TTC	263
Glu Lys Thr Leu Ser Trp Gly Cys Gly Phe Gly Leu His Ser Gly Phe	
-35 -30 -25	
GGC GGT TCC GGG GGA GGG CTC CGT CTG TGC CGA TTA CTC TGT CTT GTA	311
Gly Gly Ser Gly Gly Gly Val Gly Leu Cys Arg Leu Leu Cys Leu Val	
-20 -15 -10	
CGT TTG TTC TGC TGC TCT TCA ATA TTG TAT CAA CGC CAG AAG	353
Arg Leu Phe Cys Cys Ser Ser Ile Leu Tyr Gln Arg Gln Lys	
-5 1 5	

## (2) INFORMATION FOR SEQ ID NO: 248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..71
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..50  
id R82719  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..44  
id AA069083  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 2..34  
id R29193  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 23..52  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 10..39  
id AA158081  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 10..96  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq AALLLTATVRLSA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```
AAGTCCAAC ATG GCG GCG CCC AGC GGA GGG TGG AAC GGC GTC GGC GCG AGC   51
      Met Ala Ala Pro Ser Gly Gly Trp Asn Gly Val Gly Ala Ser
                -25                                -20

TTG TGG GCG GCG CTG CTC CTC ACT GCC ACA GTC AGA CTT TCA GGT TGT   99
      Leu Trp Ala Ala Leu Leu Thr Ala Thr Val Arg Leu Ser Ala Ser
      -15                -10                        -5                1

CCC GGC CCA                                     108
Pro Gly Pro
```

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 7..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..159  
id R24141  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 178..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 173..259  
id R24141  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 258..299  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 254..295  
                           id R24141  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 230..349  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..120  
                           id H25030  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 4..147  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.7  
                           seq LLLFFGKLLVVGG/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

ATC ATG ATC GCC ATC TAC GGG AAG AAT TTC TGT GTC TCA GCC AAA AAT	48
Met Ile Ala Ile Tyr Gly Lys Asn Phe Cys Val Ser Ala Lys Asn	
-45 -40 -35	
GCG TTC ATG CTA CTC ATG CGA AAC ATT GTC AGG GTG GTC GTC CTG GAC	96
Ala Phe Met Leu Leu Met Arg Asn Ile Val Arg Val Val Val Leu Asp	
-30 -25 -20	
AAA GTC ACA GAC CTG CTG CTG TTC TTT GGG AAG CTG CTG GTG GTC GGA	144
Lys Val Thr Asp Leu Leu Leu Phe Phe Gly Lys Leu Leu Val Val Gly	
-15 -10 -5	
GGC GTG GGG GTC CTG TCC TTC TTT TTT TTC TCC GGT CGC ATC CCG GGG	192
Gly Val Gly Val Leu Ser Phe Phe Phe Phe Ser Gly Arg Ile Pro Gly	
1 5 10 15	
CTG GGT AAA GAC TTT AAG AGC CCC CAC CTC AAC TAT TAC TGG CTG CCC	240
Leu Gly Lys Asp Phe Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu Pro	
20 25 30	
AYC ATG ACC TCC ATC CTG GGG GCC TAT GTC ATC GCC AGY GGC TTC TTC	288
Xaa Met Thr Ser Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe Phe	
35 40 45	
AGC GTT TTC GGC ATG TGT GTG GAC ACG CTC TTC CTC TGC TTC CTG GAA	336
Ser Val Phe Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu Glu	
50 55 60	
GAC CTG GAG CGG ACA ACG GCT CCC TGG ACG GCC CTA CTA CAT GTC CAA	384
Asp Leu Glu Arg Thr Thr Ala Pro Trp Thr Ala Leu Leu His Val Gln	
65 70 75	

GAG CTT CTA  
Glu Leu Leu  
80

393

## (2) INFORMATION FOR SEQ ID NO: 250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..265
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 220..263  
id N89186  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 76..348
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq SVLELIVASVCQS/HI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```

GCTACTTTCT TTTTCAGTCT TTCGGTGCGG AGAAGGGGAG GAGGCGGGCA CAGGTCTGAA   60
AAAATCGAAT GCCTT ATG GAA AGG AAC TGC AAG GGT TCC TTT GGG GTG ATC   111
      Met Glu Arg Asn Cys Lys Gly Ser Phe Gly Val Ile
      -90                      -85                      -80

AAA GAG GGA GAC ACA GAC ACA GRR GAG ACA AAG GCA AGG AGG ACT GTC   159
Lys Glu Gly Asp Thr Asp Thr Xaa Glu Thr Lys Ala Arg Arg Thr Val
      -75                      -70                      -65

TGG GAG CCA CGC GGG CGA TAC AGT TTC CGA GRM ACG CCG CGT CCC GCC   207
Trp Glu Pro Arg Gly Arg Tyr Ser Phe Arg Xaa Thr Pro Arg Pro Ala
      -60                      -55                      -50

TAT CCF GTT GAA CAG TGC GGA TTT GCG AGG CGC GCC CTG GAG CTG CTA   255
Tyr Pro Val Glu Gln Cys Gly Phe Ala Arg Arg Ala Leu Glu Leu Leu
      -45                      -40                      -35

GAG ATC CGG AAG CAC AGC CCC GAG GTG TGC GAA CCA CCA AAC ATC CCA   303
Glu Ile Arg Lys His Ser Pro Glu Val Cys Glu Pro Pro Asn Ile Pro
      -30                      -25                      -20

```

GTT ACC AGT GTC CTT GAA TTG ATA GTG GCT TCT GTT TGT CAG TCT CAT 351  
 Val Thr Ser Val Leu Glu Leu Ile Val Ala Ser Val Cys Gln Ser His  
 -15 -10 -5 1

ATA AGA ACT ACT 363  
 Ile Arg Thr Thr  
 5

## (2) INFORMATION FOR SEQ ID NO: 251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
 region 1..243  
 id AA211459  
 est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 15..212
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
 seq LYMLAEALPVSHG/AH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

GTGAAGATGA AGCC ATG TTT GTA GAA TAT AGA AAA CAA CTG AAG TTA CTG 50  
 Met Phe Val Glu Tyr Arg Lys Gln Leu Lys Leu Leu  
 -65 -60 -55

TTG GAC AGG CTT GCT CAA GTT TCA CCA GAG TTA CTA CTG GCC TCT GTT 98  
 Leu Asp Arg Leu Ala Gln Val Ser Pro Glu Leu Leu Leu Ala Ser Val  
 -50 -45 -40

CGC AGA GTT TTT AGT TCT ACA CTG CAG AAT TGG CAG ACT ACA CGG TTT 146  
 Arg Arg Val Phe Ser Ser Thr Leu Gln Asn Trp Gln Thr Thr Arg Phe  
 -35 -30 -25

ATG GAA GTT GAA GTA GCA ATA AGA TTG CTG TAT ATG TTG GCA GAA GCT 194  
 Met Glu Val Glu Val Ala Ile Arg Leu Leu Tyr Met Leu Ala Glu Ala  
 -20 -15 -10

CIT CCA GTA TCT CAT GST GCT CAC TTC TCA GGT GAT GTT TCA AAA GCT 242  
 Leu Pro Val Ser His Gly Ala His Phe Ser Gly Asp Val Ser Lys Ala



	1	5	10	
AST GCT TTG CAG GAT ATG ATG CGA ACT CTG GTA ACA TCA GGA GTC AGC				290
Ser Ala Leu Gln Asp Met Met Arg Thr Leu Val Thr Ser Gly Val Ser				
	15	20	25	
GGG				293
Gly				

## (2) INFORMATION FOR SEQ ID NO: 252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 155..187
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 95..127  
id H83489  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 326..388
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq IIFLIQWHGGSVFQ/EF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

AAGTCCCTGT ACAGGGTTTC TGACCTGTGG TAAAAACAGA ATGTCACCTTT CTGACAGGCA	60
CAGTACCCCC AGGATAAACT TGGAACTCTG AGAGGAAATT CACGAAACTC GTGGSGGCAG	120
GGGTCACAAG GTGCTTGGTG GGGGARAASC TGGAAGACAT ATTGTCCAGG AGAAGGAATG	180
TCACAAGGAA CTGACAAAAT CAAGTCACGG CGCCTACAAA GATGAGGGGC AGATTCTGGC	240
TGCCTTTTAA TTTCGTCTTT CACCTGATAT CTGTGCCAGA GAATGATAAA AATCATAATA	300
AAGGRAATAG YGGAAGAGGA GACTT ATG TTA CTG GGG ACA TCT AAC ATA ATT	352
Met Leu Leu Gly Thr Ser Asn Ile Ile	
-20 -15	
ATT TTC CTG ATT CAG TGG CAT GGT TCA GTC TTC CAG GAG TTC	394
Ile Phe Leu Ile Gln Trp His Gly Ser Val Phe Gln Glu Phe	
-10 -5 1	

## (2) INFORMATION FOR SEQ ID NO: 253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 35..225  
id HSC0CC021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..35  
id HSC0CC021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..212  
id T32119  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 36..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..203  
id T35494  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 13..202  
id HUMHG5097  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 51..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..188  
id AA027882  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 78..137  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq AFVXACVLSLIST/IY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```
AAGAGTAGGG TGCTGTGGTC TGAGCTAGAG GGTGAAGCTG GCGGASAGGA GGATGGGCGA    60
GCAGTCTGAA TGCCAGA ATG GRT AAC CGT TTT GCT ACA GCA TTT GTA ATD      110
      Met Xaa Asn Arg Phe Ala Thr Ala Phe Val Xaa
      -20                -15                -10
GCT TGT GTG CTT AGC CTC ATT TCC ACC ATC TAC ATG GCA GCC TCC ATT      158
Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile
      -5                1                5
GGC ACA GAC TTC TGG TAT GAA TAT CGA AGT CCA GTT CAA GAA AAT TCC      206
Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser
      10                15                20
AGT GAT TTG AAT AAA AGC ATC TGG GAT GAA TTG                          239
Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Leu
      25                30
```

## (2) INFORMATION FOR SEQ ID NO: 254:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(43..130)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 176..263  
id C01485

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(137..219)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 88..170  
id C01485  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 421..459
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq MSLTSGFLRVSG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```

CACCAATGTT ATGAATGGCG TGGCCTCCTA CTGCCGTCCC TGTGCCCTAG AAGCCTCTGA   60
TGTGGGCTCC TCCTGCACCT CTTGTCCTGC TGGTTACTAT ATTGACCGAG ATTCAGGAAC   120
CTGCCAMTCC BTGCCCCCCT AACACAATTC TGAAAGCCCA CCAGCCTTAT GGTGTCCAGG   180
CCTGTGTGCC CTGTGGTCCA GGGACCAAGA ACAACAAGAT CCACTCTCTG TGCTACAATG   240
ATTGCACCTT CTCACGCAAC ACTCCAACCA GGACTTTCAA CTACAACTTC TCCGCTTTGG   300
CAAACACCGT CACTCTTGCT GGAGGGCCAA GCTTCACTTC CAAAGGTTG AAATACTTCC   360
ATCACTTTAC CCTCAGTCTC TGTGGAAACC AGGGTAGGAA AATGTCTGTG TSCACCGACA   420
ATG TCA CTG ACC TCC GGA TTC CTG AGG GTG AGT CAG GGT TCT CCA AAT   468
Met Ser Leu Thr Ser Gly Phe Leu Arg Val Ser Gln Gly Ser Pro Asn
      -10                      -5                      1

CTA TCA CAG                                     477
Leu Ser Gln
5 -

```

## (2) INFORMATION FOR SEQ ID NO: 255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 55..316  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 1..262  
 id H37671  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 102..261  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 50..209  
 id N47067  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 55..104  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 2..51  
 id N47067  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 251..316  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 14..79  
 id AA135001  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 58..246  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.6  
 seq AIRTLFSVTGILA/EQ

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

AACTTGGCGC GCGGCSSGGC TGCAGACGGC TGCGAGGCGC TGGGCACAGG TGTCCCTG	57
ATG GCA AAT TTC AAG GGC CAC GCG CTT CCA GGG AGT TTC TTC CTG ATC	105
Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile	
-60 -55 -50	
ATT GGG CTG TGT TGG TCA GTG AAG TAC CCG CTG AAG TAC TTT AGC CAC	153
Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His	
-45 -40 -35	
ACG CGG AAG AAC AGC CCA CTA CAT TAC TAT CAG CGT CTC GAG ATC GTC	201
Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val	
-30 -25 -20	
GAA GCC GCA ATT AGG ACT TTG TTT TCC GTC ACT GGG ATC CTG GCA GAG	249
Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu	
-15 -10 -5 1	

CAG TTT GTT CCG GAT GGG CCC CAC CTG CAC CTC TAC CAT GAG AAC CAG 29  
Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His  
5 10 15  
TGG ATA AAG TTA ATG AAT 315  
Trp Ile Lys Leu Met Asn  
20

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 84..400  
id N34255  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..84  
id N34255  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..304
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 83..298  
id H79944  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..54
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 2..48  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 336..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 332..378  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 304..340
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 299..335  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..83
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 49..83  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 109..298
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 106..295  
id H73369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..87  
id H73369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 336..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 336..382  
id H73369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 295..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 293..324  
id H73369

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 164..237  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 142..215  
id AA132425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 327..395  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 307..375  
id AA132425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..88  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 3..70  
id AA132425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..163  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 103..142  
id AA132425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 109..298  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 24..213  
id R97376  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 296..405  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 212..321  
id R97376  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 187..342  
(C) IDENTIFICATION METHOD: Von Neijne matrix  
(D) OTHER INFORMATION: score 5.5



seq AGLLEKSLAGLGA/YQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```

AGCAGGCACA ACAGAGCCGC TCCCWCTCC TCGCCCCGCC ACCGGGACGG AGAGCGCCCG   60
CGGCTGCATT TCGGGCGACA CCTCGCAGGT CATTCCTGCG GCTTGGCGCG CTTGTAGAC   120
AGCGGGGGCC TTCGTSAGAC CGGTGCAGGC CTGGGGTAST CTTGTCTCTG GACAGAGAAG   180
AGAAAA ATG CAG GAC ACT GGC TCA GTA GTG CTT TTG CAT TGG TTT GGC   228
      Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly
            -50                -45                -40

TTT GGC TAC GCA GCA CTG GTT GCT TCT GGT GGG ATC ATT GGC TAT GTA   276
Phe Gly Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val
            -35                -30                -25

AAA GCA GGC AGC GTG CCG TCC CTG CCT GCA GGG CTG CTC TTT GGC AGT   324
Lys Ala Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser
            -20                -15                -10

CTA GCC GGC CTG GGT GCT TAC CAG CTG TCT CAG GAT CCA AGG AAC GTT   372
Leu Ala Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val
            -5                1                5                10

TGG GTT TTC CTA GCT ACA TCT GGT ACC TTG GCT   405
Trp Val Phe Leu Ala Thr Ser Gly Thr Leu Ala
            15                20

```

(2) INFORMATION FOR SEQ ID NO: 257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 119..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 116..234  
id HSC2TH021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 24..94  
id HSC2TH021  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 238..289  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 234..285  
id HSC2TH021  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 280..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 277..316  
id HSC2TH021  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..237  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 23..130  
id R59681  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 238..289  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 130..181  
id R59681  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 280..325  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 173..218  
id R59681  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 183..287  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.4  
seq CCALLTSLXCIWG/PA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

ACCTTCTGTI ACTGTCCGGG GCTGCGGGGC TTGCTTCKG CGTCAWGGCT CAAAGGGCCT 60

```

TCCCGMATCC TTATGCTGAT TATAAGAAAT CCCTGDRCCG AAGSTACTTT GATGCTGCCG 120
GGARGCTGAC TCCTGASTTC TCACAACGCT TSACCAATAA GATTCGGGAG CTTCTTCAGC 180
AA ATG GAG AKA GGC CTG AAA TCA GCA GAC CCT CGG GAT GGC ACC GGT 227
  Met Glu Xaa Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly
  -35                -30                -25

TAC ACT GRC TTN NKC ARG TAT TGC TGT GCT TTA CTT ACA TCT TTA TGR 275
Tyr Thr Xaa Xaa Xaa Xaa Tyr Cys Cys Ala Leu Leu Thr Ser Leu Xaa
-20                -15                -10                -5

TGT ATT TGG GGA CCT CCC TAC CTA CAG TTA GCA CAT GGC TAT GTA AAG 323
Cys Ile Trp Gly Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys
      1                5                10

```

## (2) INFORMATION FOR SEQ ID NO: 258:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 12..252  
id H64050  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..241  
id R17172  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 2..242  
id HSC15C081  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 8..241  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..234  
id AA149663  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 29..241  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 29..241  
id HSJ46380  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 10..135  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.4  
seq ITGVILLAVGIWG/KV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```
GGGCTASTC ATG GCG TCC CCG TCT CGG AGA CTG CAG ACT AAA CCA GTC ATT    51
Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile
      -40                      -35                      -30

ACT TGT TTC AAG AGC GTT CTG CTA ATC TAC ACT TTT ATT TTC TGG ATC    99
Thr Cys Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile
      -25                      -20                      -15

ACT GGC GTT ATC CTT CTT GCA GTT GGC ATT TGG GGC AAG GTG AGC CTG   147
Thr Gly Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu
      -10                      -5                      1

GAG AAT TAC TTT TCT CTT TTA AAT GAG AAG GCC ACC AAT GTC CCC TTC   195
Glu Asn Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe
      5                      10                      15                      20

GTG CTC ATT GCT ACT GGT ACC GTC ATT ATT CTT TTG GGC ACC TTG     240
Val Leu Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Leu
      25                      30                      35
```

## (2) INFORMATION FOR SEQ ID NO: 259:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 6..347  
id AA075824  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 344..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 341..382  
id AA075824  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..346  
id R55598  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..315  
id HSC33B061  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 91..320  
id T65515  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..141
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 5..76  
id T65515  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..305
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..273

Id HSCZRF061  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 119..319
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LSVSLLEPCAGAWS/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```

AAAAGCGGAG MYAGGMNCGG TGAGGAGAGT CGAGGGAGGT GACGCGCGCT GCCGGGGCGA    60
GGTTGCGAGG GSCGGTGTG AAGAATGTGT GGGCGAACAT CCTGTCACCT ACCTAGAG    118
ATG TTC TCA CGA GAG CTT GCG CCT ACC AGG ATC GGC GGG GCC AGC AGC    166
Met Phe Ser Arg Glu Leu Ala Pro Thr Arg Ile Gly Gly Ala Ser Ser
   -65                      -60                      -55
GGC TCC CGG AGT GGA GGG ACC CTG ATA AGT ACT GCC CCT CTT ACA ACA    214
Gly Ser Arg Ser Gly Gly Thr Leu Ile Ser Thr Ala Pro Leu Thr Thr
   -50                      -45                      -40
AGA GTC CTC AAT CCA ACA GCC CAG TGC TTC TGT CTC GAC TGC ACT TTG    262
Arg Val Leu Asn Pro Thr Ala Gln Cys Phe Cys Leu Asp Cys Thr Leu
   -35                      -30                      -25                      -20
AGA AGG ATG CAG ACT CAT CTG AGC GTA TCA TTG CTC CCA TGC GCT GGG    310
Arg Arg Met Gln Thr His Leu Ser Val Ser Leu Leu Pro Cys Ala Gly
   -15                      -10                      -5
GCT TGG TCC CTT CTT RGT TCA AAG AAA GTG ATC CTT CCA AGC TGC AGT    358
Ala Trp Ser Leu Leu Xaa Ser Lys Lys Val Ile Leu Pro Ser Cys Ser
      1                      5                      10
TCA ATA CTA MCA ACT GTC GTA GTG ATA    385
Ser Ile Leu Xaa Thr Val Val Val Ile
   15                      20

```

## (2) INFORMATION FOR SEQ ID NO: 260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..123
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 13..104  
id R49759  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 132..194  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 106..168  
id R49759  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 225..311  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq LLMLGVILPNSYW/RV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```

ATTCTCTGA CCTGCCAGGA AGCAGAGAGA CCCACAGAGC AGGCAGGGAG GCAGAAAGTG   60
GAGACGGACC TGAGCCCGAG GAAGAGGCAG GCAGAGGCTG AGGCTGATTC CACCCCAGCC   120
TGCCTGGRAC AAACCTCCT TAGCCGCAGC CCCTTCCAST TCCCTAGGGG TTCTGCCCTT   180
CCCCCTCTCT GGGGCACCAG CCCCCAGGG TCCTGCATCC NACC ATG TCG ATG GCT   236
                               Met Ser Met Ala

GTG GAA ACC TTT GGC TTC TTC ATG GCA ACT GTG GGG CTG CTG ATG CTG   284
Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly Leu Leu Met Leu
-25          -20          -15          -10

GGG GTG ACT CTG CCA AAC AGC TAC TGG CGA GTG TCC ACT GTG CAC GGG   332
Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser Thr Val His Gly
          -5              1              5

AAC GTC ATC AHC ACC AAC AHC ATC TTC GAG AAC CTC TGG TTT AGC AGT   380
Asn Val Ile Xaa Thr Asn Xaa Ile Phe Glu Asn Leu Trp Phe Ser Ser
          10              15              20

GCC GGG   386
Ala Gly
  25

```

## (2) INFORMATION FOR SEQ ID NO: 261:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (D) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 112..216  
id T86663  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 120..153  
id AA055880  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 55..114
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq XFLXLXXLSXXWP/XD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```

ACTCAGAAGC TTGGACCGCA TCCTAGCCGC CGACTCACAC AAGGCAGABT TGCC ATG      57
                                     Met
                                     -20

GAG AAA ATT CCA GTG TCA SCA TTC TTG CDC CTN GYG GSC CTC TCK WAS      105
Glu Lys Ile Pro Val Ser Xaa Phe Leu Xaa Leu Xaa Xaa Leu Ser Xaa
      -15                      -10                      -5

AKC TGG CCA SSG GAT ACC ACA GTC AAA CCT GGA GCC AMA AAG GAC ACA      153
Xaa Trp Pro Xaa Asp Thr Thr Val Lys Pro Gly Ala Xaa Lys Asp Thr
      1                      5                      10

AAG GAC TCT CGA SCC AAA CTG CCC CAG ACC CTC TCC AGA GGT TGG GGT      201
Lys Asp Ser Arg Xaa Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly
      15                      20                      25

GAC CAA CTC ATC TGG ACA CGG                                          222
Asp Gln Leu Ile Trp Thr Arg
      30                      35

```

## (2) INFORMATION FOR SEQ ID NO: 262:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 207..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 85..204  
id W69716  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 122..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..87  
id W69716  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 316..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 195..245  
id W69716  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 282..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 94..178  
id W73842  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 207..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 17..97  
id W73842  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 257..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 42..111  
id W58103  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 317..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 101..150  
id W58108  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 112..312
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq LILERPLVPSAEA/SG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

ATAAGGCCTC AGGSTCCTGT TTTCCTGGC CTCTTCTAGA GGGCCCGTGG AMCAGGTGGC      60
AGTGGCGTGT TATTTGAAAA CCAGSTGTGT GAGCCGAATG CCTGCCAGGC C ATG CAC      117
                               Met His

TCA GCA GAG GAG CCC TTG TAN CTG GCT GCC CTG AGA GGA GCA AGA GGC      165
Ser Ala Glu Glu Pro Leu Xaa Leu Ala Ala Leu Arg Gly Ala Arg Gly
-65                -60                -55                -50

CAC CTC CCA TGT GGC TCT AGA CAC CAC GTG GGC TCA TTA GCC CCA GCG      213
His Leu Pro Cys Gly Ser Arg His His Val Gly Ser Leu Ala Pro Ala
                -45                -40                -35

TCT GTG CCG GCT CCA GGT GCC TGC CTC TGG GTG TGT GAG TGG GAG ACT      261
Ser Val Pro Ala Pro Gly Ala Cys Leu Trp Val Cys Glu Trp Glu Thr
                -30                -25                -20

TTG CTC CCT GGC CTC ATC CTA GAG AGG CCC CTG GTG CCT AGT GCT GAG      309
Leu Leu Pro Gly Leu Ile Leu Glu Arg Pro Leu Val Pro Ser Ala Glu
                -15                -10                -5

GCC TCT GGG GCT GGA AAG CTC AGC AGA AAG GAG GCA CTA CTG AGC AAC      357
Ala Ser Gly Ala Gly Lys Leu Ser Arg Lys Glu Ala Leu Leu Ser Asn
                1                5                10                15

TAT GCA TTG      366
Tyr Ala Leu

```

## (2) INFORMATION FOR SEQ ID NO: 263:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 121..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 127..270  
id N24991  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 3..124  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 10..131  
id N24991  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 161..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 15..146  
id HSC1WG111  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 176..310  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..135  
id AA001396  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 176..265  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..90  
id AA017578  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 191..265  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..75  
id R17530  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 167..295  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.9

seq GLWLALVDGLVRX/AP

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

ACTTTTTCCT ACGCAGCCGC TCCTGCCGEC GTGGTCGCTG GAGCTTTGCC TCTCTAGGCC      60
GGCAGCGCCT CTCTCCATG GTCCTGTCTG TCAGCGCTGT TTTGCGAGCC CCGCGGTGAG      120
CCCGGGCCAC GCTCAGACAC TTCGATCGTC GAGTCTGTCA CTGGGG ATG GCG GGT      175
                               Met Ala Gly
CAG TTC CGC AGC TAC GTG TGG GAC CCG CTG CTG ATC CTG TCG CAG ATC      223
Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu Ser Gln Ile
-40          -35          -30          -25
GTC CTC ATG CAG ACC GTG TAT TAC GGC TCG CTG GCG CTG TGG CTG GCG      271
Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala
          -20          -15          -10
CTG GTG GAC GGG CTA GTG CGA ASA GCC CCT CGC TGG ATC SCA GCG      316
Leu Val Asp Gly Leu Val Arg Xaa Ala Pro Arg Trp Ile Xaa Gly
          -5          1          5

```

(2) INFORMATION FOR SEQ ID NO: 264:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 76..316  
id W03477  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..78
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 7..83  
id W03477  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..328

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 69..325  
id W40364  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 3..78  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..76  
id W40364  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 164..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 172..336  
id R71313  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 72..158  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 80..166  
id R71313  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 7..78  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 16..87  
id R71313  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 164..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 151..315  
id H87810  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 72..158  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 59..145  
id H87810  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 14..78  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 2..66  
id H87810  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 72..274  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 52..254  
id AA135694  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 20..78  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..59  
id AA135694  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 270..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 249..307  
id AA135694  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 62..295  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.9  
seq VGAVFGLTTCISA/HV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```
AGGCTGCCCT TCGCTTCCC GAGCTGGCGG GGTCCGTGGT GCGGGATCGA GATTGCGGGC   60
T ATG GCG CCG AAG GTT TTT CGT CAG TAC TGG GAT ATC CCC GAT GGC ACC   109
  Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr
    -75                      -70                      -65

GAT TGC CAC CGC AAA GCC TAC AGC ACC ACC AGT ATT GCC AGC GTC GCT   157
Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala
  -60                      -55                      -50

GGC CTG ACC GCC GCT GCC TAC AGA CTC ACA CTC AAT CCT CCG GGC ACC   205
Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
  -45                      -40                      -35

TTC GTT GAA GGA GTG GCT AAG GTT GGA CAA TAC ACG TTC ACT GCA GCT   253
Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
```

-30                      -25                      -20                      -15

GCT GTC GGG GCC GTG TTT GGC CTC ACC ACC TGC ATC AGC GCC CAT GTC      301  
Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val  
                    -10                      -5                      1

CCC GAG AAG CCC GAC GAC CCC CTG AAC CGG                      331  
Arg Glu Lys Pro Asp Asp Pro Leu Asn Arg  
                    5                      10

## (2) INFORMATION FOR SEQ ID NO: 265:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(44..183)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..140  
id N78549  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..34)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 150..182  
id N78549  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(103..214)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 100..211  
id N27605  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 150..203
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq WLQVLPVILLLLG/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```

AGAGAGAGGG GCCGCTACGC CGCACAGCAA ACAAGCTCCG CGACGTTTCC AGGACCCGGA    60
TAATCCCGCC CTTAGAGCAG AGCCGGAAGA AGSCGGGACG AACCGGAAGA GGGTGAATG    120
CITTCGGTAG GCACTCCACG GCTGTGAAG ATG GCG GCG GCT GCG TGG CTT CAG    173
                               Met Ala Ala Ala Ala Trp Leu Gln
                               -15

GTG TTG CCT GTC ATT CTT CTG CTT CTG GGA GTC CCC CCG TCS            215
Val Leu Pro Val Ile Leu Leu Leu Leu Gly Val Pro Pro Ser
-10                               -5                               1

```

## (2) INFORMATION FOR SEQ ID NO: 266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 59..182  
id AA045287  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 45..168  
id R77973  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 70..193  
id AAL36043  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn



(D) OTHER INFORMATION: identity 100  
region 60..183  
id AA115201  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..124)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 60..183  
id R72616  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 5..115  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.3  
seq LLILDMNVLYTDA/SP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

ATAG ATG GAA ATA TAC TTT ATA TTT TGT ATC ATC GTG CCT ATA GCC GCT	49
Met Glu Ile Tyr Phe Ile Phe Cys Ile Ile Val Pro Ile Ala Ala	
-35 -30 -25	
GCC ACC GTG TAT AAA TCC TGG TGT CTG CTC CTT ATC CTG GAC ATG AAT	97
Ala Thr Val Tyr Lys Ser Trp Cys Leu Leu Leu Ile Leu Asp Met Asn	
-20 -15 -10	
GTA TTG TAC ACT GAC GCG TCC CCA CTC GGG	127
Val Leu Tyr Thr Asp Ala Ser Pro Leu Gly	
-5 1	

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 36..128  
id AA054941  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..197  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 117..184  
id AA054941  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..218  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 36..206  
id W68324  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..141  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 22..115  
id H72703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..218  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 103..191  
id H72703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 29..59  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 4..34  
id H72703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 16..108  
id AA128297  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..218  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 97..135  
id AA128297

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..141  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 13..106  
id W25240  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..218  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 94..182  
id W25240  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 71..163  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq VLLAIGMFFIAWF/FV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```
ACTGTCGACG TGTTCTTCCG GTGGCGGACG GCGGATTAGC CTTCGCGGGG CAAAATTGRA      60
RCYCDRGGCC ATG AGC AGA TAT ACC AGC CCA GTG AAC CCA GCT GTC TTC      109
      Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe
      -30                -25                -20

CCC CAT CTG ACC GTG GTG CTT TTG GCC ATT GGC ATG TTC TTC ACC GCC      157
Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala
      -15                -10                -5

TGG TTC TTC GTT TAC GAG GTC ACC TCT ACC AAG TAC ACT CGT GAT ATC      205
Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile
      1                5                10

TAT AAA GAG CTC CAG                                          220
Tyr Lys Glu Leu Gln
      15
```

## (2) INFORMATION FOR SEQ ID NO: 268:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..179  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 15..59  
id R68571  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 309..413  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq LMLSSSLPLLIWL/KD

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```

AACTTTAGCC TCTGATTGCA GGCCACCACT TCATTACAT GGGGTGAGCA CCAATGCGTT    60
TTGTTCAATT CTTTGTTCAA AACCCCAAGA ATCTGGACAA CTTGCACTCA AGACCCCTCA    120
CGGGTTTGGC GAGCCAGTCC TTCAGTGGCT GTTTTCTAGT AGCTCCTTGG CAATTGAGGG    180
GAAGTGGCTG GGACCACTCT CCAGTGCTGT CTGAAGGCCA AGGAGTGAAC AGGGATGGCT    240
GCCCTGCCTT GAAGAGGGAA GGAATCTTTT CTATCCTTTC CAGCTATAGT CCCTGATCCC    300
TACATGTG ATG CGG TTG GCA GCG GAA GCT CAT CCT GGG CGA ACT CAC ACA    350
Met Arg Leu Ala Ala Glu Ala His Pro Gly Arg Thr His Thr
-35                      -30                      -25

CTT TTC AGG AGA CTT AAA CCT TTT CTT ATG CTA AGT TCT TCC CTT CCC    398
Leu Phe Arg Arg Leu Lys Pro Phe Leu Met Leu Ser Ser Ser Leu Pro
-20                      -15                      -10

CTA CTC ATC TGG CTA AAG GAC AGA                                422
Leu Leu Ile Trp Leu Lys Asp Arg
-5                      1

```

## (2) INFORMATION FOR SEQ ID NO: 269:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 17..276  
id N23506  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..220  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 8..226  
id R74310  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 219..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 226..268  
id R74310  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 103..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 125..283  
id N42319  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 103..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 119..277  
id N33735  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 105..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 143..299  
id R23867  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 97..213  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq IILFSAIVGFIYG/YV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

AAATGCCRRR CATTAGCCCT CACGGTCCTT AAGTCTCGGT CGCCCTCGCC TCKCAGCCTG   60
CCVBCCGCCG TCRKCTGSSC GACTCCTCAG SCAGCC ATG CTG GAG CAT CTG RGC   114
                                         Met Leu Glu His Leu Xaa
                                         -35

TCG CTG CCC ACC CAG ATG GAT TAC AAG GGC CAG AAG CTA CCT GRR CAG   162
Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly Gln Lys Leu Ala Xaa Gln
-30 -25 -20

ATG TTT CAG GGR ATT ATT CTT TTT TCT GCA ATA GTT GGA TTT ATC TAC   210
Met Phe Gln Gly Ile Ile Leu Phe Ser Ala Ile Val Gly Phe Ile Tyr
-15 -10 -5

GGG TAC GTG GCT GAA CAG TTC GGG TGG ACT GTC TAT ATA GTT ATG GCC   258
Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr Val Tyr Ile Val Met Ala
1 5 10 15

GGA   261
Gly

```

## (2) INFORMATION FOR SEQ ID NO: 270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(154..354)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 70..270  
id AA164185  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..111
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 298..381  
id AA164184  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 297..344
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8  
seq SKVLPSFNVLG/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```

CCAACGTGTG CTTTGAAAAA AAGAAGGGAT GTTTTCTGTS TCAATGAAG STAATCATAG   60
ATCAAATTTG CTTATTGTCT TGTTCAAATC CTAGAAAACC ATTAGCATTT TTCTTTGCTT  120
GTAATATKAG AATCTAACAC TCATACAGAA TATTGGAAG GTTACCCTAC AATTGTAAAT  180
TTGAAATTCT CCTTCTAATT CTGTCAGTTA TTTATTGACA TAGTAGTGGT TCTGTAGTCA  240
AGTGCATATA AGSTTTTGAA TGTTACATCT TATTNNNGGA TTWTTATTTT ATCATT ATG   299
                                         Met
GAG TAT AGC AAA GTT CTA TTT TGT TCT TTT TCA AAT GTA CTT GGT TTT   347
Glu Tyr Ser Lys Val Leu Phe Cys Ser Phe Ser Asn Val Leu Gly Phe
-15              -10              -5              1

GAT TAT                                         353
Asp Tyr

```

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..133
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..115  
id HSC13B041  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 105..207  
id HSC13B041  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..226

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 71..173  
id T08849  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..133  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..81  
id T08849  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..135  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..83  
id H88132  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..192  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 71..139  
id H88132  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 192..226  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 140..174  
id H88132  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..144  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..92  
id T33149  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 145..226  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 92..173  
id T33149  
est

(ix) FEATURE:



(A) NAME/KEY: other  
 (B) LOCATION: 52..133  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 1..82  
                           id AA121114  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 192..226  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 141..175  
                           id AA121114  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 46..123  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
                           seq LIMQLGSVLLTRC/PF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```

ACTCTCTGAC TGGGGTGAGG CCGCAGCGGA CTGCCCTTTC CSAAG ATG GCG TCG AAG    57
                                   Met Ala Ser Lys
                                   -25

ATA GGT TCG AGA CGG TGG ATG TTG CAG CTG ATC ATG CAG TTG GGT TCG    105
Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met Gln Leu Gly Ser
      -20                      -15                      -10

GTG CTG CTC ACA CGC TGC CCC TTT TGG GGC TGC TTC AGC CAG CTC ATG    153
Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe Ser Gln Leu Met
      -5                      1                      5                      10

CTG TAC GCT GAG AGG GCT GAG GCA CGC CGG AAG CCC GAC ATC CCA GTG    201
Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro Asp Ile Pro Val
      -          15                      20                      25

CCT TAC CTG TAT TTC GAC AGT GGG                                225
Pro Tyr Leu Tyr Phe Asp Ser Gly
      30
  
```

## (2) INFORMATION FOR SEQ ID NO: 272:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..287  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 9..294  
id W52125  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..283  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..265  
id AA024623  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 22..284  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..263  
id H55824  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 2..288  
id R62921  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 102..287  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 57..242  
id N31702  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..100  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..56  
id N31702  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 69..224  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7

seq LGLALGRLEGGSA/RH

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

ATTGGCTCCG GATCGTGGCT GAGGCGGCTT CGTGGGCAGC GAGAGTCACA GACAAGACAG    60
CAAGCAGG ATG GAG CAC TAC CGG AAA GCT GGC TCT GTA GAG CTC CCA GCG    110
      Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala
            -50                -45                -40
CCT TCC CCA ATG CCC CAG CTA CCT CCT GAT ACC CTT GAG ATG CGG GTC    158
Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val
            -35                -30                -25
CGA GAT GGC AGC AAA ATT CGC AAC CTG CTG GGG TTG GCT CTG GGT CGG    206
Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg
            -20                -15                -10
TTG GAG GGC GGC AGT GCT CGG CAT GTA GTG TTC TCA GGT TCT GGC AGG    254
Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg
            -5                1                5                10
GCT GCA GGA AAG GCT GTC AGC TGC GCT GAG ATT GTC AAG CGG CGG GTC    302
Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val
            15                20                25
CCG    305
Pro

```

(2) INFORMATION FOR SEQ ID NO: 273:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 2..213  
id W26501  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 6..219

id W28013  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(211..324)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 334..447  
id W28077  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 215..324  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..110  
id HSC3LG011  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 104..181  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq LIALTCLDGTTVS/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```

AGCATTTTGC AAAGATGGCT GTAGGAATGG AGGAGCCTGT ATTGCCGCTA ATGTGTGTGC      60
CTGCCCCACAA GGCTTCACTG GACCCAGCTG TGAAACGACA TTG ATG AAT GCT CTG      115
                                     Met Asn Ala Leu
                                     -25

ATG GTT TTG TTC AAT GTG ACA GTC GTG CTA ATT GCA TTA ACC TGC CTG      163
Met Val Leu Phe Asn Val Thr Val Val Leu Ile Ala Leu Thr Cys Leu
-20                               -15                               -10

GAT GGT AGC ACT GTG AGT GCA GAG ATG GCT ACC ATG ACA ATG GGA TGT      211
Asp Gly Thr Thr Val Ser Ala Glu Met Ala Thr Met Thr Met Gly Cys
-5                               1                               5                               10

TTT CAC CAA GTG GAG AAT CGT GTG AAG ATA TTG ATG AGT GTG GCA CCG      259
Phe His Gln Val Glu Asn Arg Val Lys Ile Leu Met Ser Val Gly Pro
15                               20                               25

GGA GGC ACA GCT GTG CCA ATG ATA CCA TTT GCT TCA ATT TGG ATG GCG      307
Gly Gly Thr Ala Val Pro Met Ile Pro Phe Ala Ser Ile Trp Met Ala
30                               35                               40

GAT ATG ATT GNC GAT      322
Asp Met Ile Xaa Asp
45

```

## (2) INFORMATION FOR SEQ ID NO: 274:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(v1) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 94..339  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 62..307  
id AA133635  
est

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 32..97  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..66  
id AAL33635  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 191..325  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq VLVYLVTAEKRWSD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

ACTCCCAGGC	TGGGCCAGCA	CACCCGGCAG	GCTCTGTCCT	GGAAACAGGC	TTCAACGGGC	60
TTCCCCGAAA	ACCTTCCCCG	CTTCTGGRTA	TGAAVWTKCA	AGCTGCTTGC	TGAGTCCTAT	120
TGCCGGCTGC	TGGGAGCMAG	GAGAGCCCTG	AGGAGTAGTC	ACTCAGTAGC	AGCTGACGGC	180
TGGGTCCACC	ATG AAC TGG AGT ATC TTT GAG GGA CTC CTG AGT GGG GTC	228				
	Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val					
	-45 -40 -35					
AAC AAG TAC TCC ACA GCC TTT GGG CGC ATC TGG CTG TCT CTG GTC TTC	276					
Asn Lys Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe						
-30 -25 -20						
ATC TTC CGC GTG CTG GTG TAC CTG GTG ACG GCC GAG CGT GTG TGG AGT	324					
Ile Phe Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser						
-15 -10 -5						
GAT GAC CAC AAG	332					
Asp Asp His Lys						

## (2) INFORMATION FOR SEQ ID NO: 275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 37..119  
id T82645  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 129..176
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq SLFIYIFXTCSNT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

```

ACTGTCCCAT TCCTCCCCCT ACAACACACA CACCTTTCAG GCAGGGASGN GATGAGCTTC   60
CAGCCCCAAG AGTGGAGGCT GCCACATCCT AACATASGKA KCTATTGRRR AGGAAKSAGT  120
GTGTATCT ATG ATT ATA TCT CTG TTC ATC TAT ATA TTT TTK ACA TGT AGC   170
Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Xaa Thr Cys Ser
  -15                      -10                      -5

AAC ACC TCT CCA TCT TAT CAA KGA ACT CAA CTC GGT CTG GGT CTC CCC   218
Asn Thr Ser Pro Ser Tyr Gln Xaa Thr Gln Leu Gly Leu Gly Leu Pro
   1                      5                      10

AGT GCC CAG TGG TGG CCT TTG ACA GGT AGG AGG ATG CAG TGC TGC AGG   266
Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg
  15                      20                      25                      30

CTA TTT TGT TTT KTG TTA CAA                                     287
Leu Phe Cys Phe Xaa Leu Gln
      35

```

## (2) INFORMATION FOR SEQ ID NO: 276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 40..195  
id AA227366  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 4..159  
id AA069390  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..152
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..144  
id AA248850  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..78  
id AA248912  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 70..114  
id AA248912  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 61..108
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4

seq LNSLSALAEAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

```
ATGGCTGTCA GAGGTGGGCG GCTTTGACCG AGAGGCTGCT GGAGCTCGTG TTTGGACGCG    60
ATG TTT CGT CTG AAC TCA CTT TCT CCT TTG GCA GAA CTG GCT GTG GGT    108
Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
   -15                -10                -5

TCT CGA TGG TAC CAT GGA GGA TCA CAG CCC ATC CAG ATC CGG CGG AGA    156
Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Arg Arg
   1                5                10                15
```

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 69..301  
id R99696  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..98
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..70  
id R99696  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 206..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 164..288  
id W90165  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..209



(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 55..166  
id W90165  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 43..98  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..56  
id W90165  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 98..330  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 82..314  
id H91200  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 16..98  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..83  
id H91200  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 98..249  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 62..213  
id R06513  
est

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 238..288  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq TLRTWLCCAGSWA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```
ACATACTTGC AGCTARAAC T AAATATTGCT GCTTGGGGAC CTCCTTCTAG CCTTAAATTT 60
CAGCTCATCA CCTTCACCTG CCTTGGTCAT GGCTCTGSCT ATTCTCCTTG ATCCTTGCCA 120
TTTGCACCAG ACCTGGATTG CTAGCGTCTC VATCTGGAGT GCGGCTGGTG GGGGGCCTGC 180
ACCGCTGTGA AGGGCGGGTG GAGGTGGAAC AGAAAGGCCA GTGGGGCACC GTGTGTG 240
ATG ACG GCT GGG ACA TTA AGG ACG TGG CTG TGT TGT GCC GGG AGC TGG 300
```

Met Thr Ala Gly Thr Leu Arg Thr Trp Leu Cys Cys Ala Gly Ser Trp  
 -15 -10 -5

GCT GTG GAG CTG CCA GCG GAA CCC CTA GTG GTA TTT TGT AWG ACC ACC 333  
 Ala Val Glu Leu Pro Ala Glu Pro Leu Val Val Phe Cys Xaa Ser Thr  
 1 5 10 15

AGC AGA AAA AGA GCA AAA GGT CTC ATC CAA TCA GTC 366  
 Ser Arg Lys Arg Ala Lys Gly Leu Ile Gln Ser Val  
 20 25

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..99)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
 region 99..196  
 id AA088690  
 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..187)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
 region 12..112  
 id AA088690  
 est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 111..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
 seq RLLVILCVSVKAG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

ACTACAGCAT GGCCACGTGG AGGCAGCGGC AGGAGAAAAA GCAGCTGGGC TTCTTCTGAA 60  
 CCCAAGCCCT CTCGACTGCC CCTATCCCTT GGAACCCCAA CATACCTACA ATG CTG 116  
 Met Leu  
 GGG AGG CCC TGC TTC CAC TCC CCG CAG AGG CTT TTG GTC ATC CTC TGC 164

Gly Arg Pro Cys Phe His Ser Pro Gln Arg Leu Leu Val Ile Leu Cys  
-20 -15 -10

GTG TCA GTA AAA GCA GGC AGC ACG  
Val Ser Val Lys Ala Gly Ser Thr  
-5 1

188

## (2) INFORMATION FOR SEQ ID NO: 279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 106..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 119..274  
id AA280906  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..112  
id AA280906  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 260..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 272..303  
id AA280906  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 224..375  
id HUM406F04B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 12..112  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..101  
id HUM406F04B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 106..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 94..128  
id HUM406F04B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 132..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 124..253  
id AA133362  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 5..92  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..88  
id AA133362  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 260..291  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 251..282  
id AA133362  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 106..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 94..249  
id N57260  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 10..92  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..83  
id N57260  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 260..291  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 247..278  
 id N57260  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 41..234  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 42..235  
 id W25567  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 1..40  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..40  
 id W25567  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 194..277  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.2  
 seq LQFVLPVATQIQQ/EV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

```

AGGGGCGGTG GGAACGGTTG TAGGACGIGG CTCTTTATTC GTGAGTTTTC CATTTACCTC   60
CGCTGAACCT AGAGCTTCAG ACGCCCTATG GCGTCCGCCT CGACACCAAC CGGCGGCCTT   120
GAGCGCTGAG CAAGCAAAGG TGGTCCTCGC GGAGGTGATC CAGGCGTTCT CCGCCCCGGA   180
GAATGCAGTG CGC ATG GAC GAG GCT CGG GAT AAC GCC TGC AAC GAC ATG       229
      Met Asp Glu Ala Arg Asp Asn Ala Cys Asn Asp Met
      -25                               -20

GGT AAG ATG CTG CAA TTC GTG CTG CCC GTG GCC ACG CAG ATC CAG CAG       277
Gly Lys Met Leu Gln Phe Val Leu Pro Val Ala Thr Gln Ile Gln Gln
-15                               -10                               -5

GAG GTT ATC AAA                                                         289
Glu Val Ile Lys
1

```

## (2) INFORMATION FOR SEQ ID NO: 280:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 base pairs

(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 38..69  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..32  
id H56508  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 237..349  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq LCALGSAPSSMWA/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
AAACCTCCGT GGCTAGTCTT GACGTGGCGG GTTGCTTTCC AAAATGGCGC GGGTGCTGAA   60
GGCTGCAGCC GCDBAATGCC GTAGGTGAAT ACCGGGCACC GCCGACCTTC GCCATGGGAC   120
AGGGAGCGTG GGAACGGCGG TCGGGGGCGG AGGAKGCCTC GGTGTGGCCA AAGCACCTTG   180
ATCTAATGTC CTCCCCGGG GCGCGTTC ACAGCAGCTG CTGTCACTTW KGGCAGAGGG   240
TGCCTTCCAG AAGCGCCACC GCTTAGTAGC GGGGATTGCB TTGTGC ATG AGT CCC   295
                               Met Ser Pro
                               -20
ATT TCG ATC CGA GAG CTG TGC GCC TTG GGC TCT GCA CCT TCC AGT ATG   343
Ile Ser Ile Arg Glu Leu Cys Ala Leu Gly Ser Ala Pro Ser Ser Met
      -15                -10                -5
TGG GCB GGA GAG   355
Trp Ala Gly Glu
      1
```

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..149  
id AA095592  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..105
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 219..306  
id T70757  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 37..129  
id H66541  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 37..129  
id R92835  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 172..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 14..97  
id H87601  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 52..90
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq MTDLLSASPWALT/IV

## (x) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

ACCAA5TTTG ACCACCTGGA AAGGGTTTAT GCTGACATCC CCTTCTGTG G ATG ACC 57  
Met Thr

```

GAC CTC TTA AGT GCC TCA CCC TGG GCC CTC ACT ATT GTT TCC AGT GAG      105
Asp Leu Leu Ser Ala Ser Pro Trp Ala Leu Thr Ile Val Ser Ser Glu
-10                               -5                               1                               5

CTC CAC CTT GCT CCA TCC ATG ACC ACA GTG CAC CAG CTC GAG TCT CAA      155
Leu His Leu Ala Pro Ser Met Thr Thr Val Asp Gln Leu Glu Ser Gln
                               10                               15                               20

GTG GAC AAT GTC ATC TTA CAG ACT GGA GAG AGT GCT AGT GAA TGC TTT      201
Val Asp Asn Val Ile Leu Gln Thr Gly Glu Ser Ala Ser Glu Cys Phe
                               25                               30                               35

TGT CTT CAA TGC CCA TCT CTT GGA AAT ATT GAA GGT GGA GTA GCA ACC      249
Cys Leu Gln Cys Pro Ser Leu Gly Asn Ile Glu Gly Gly Val Ala Thr
                               40                               45                               50

GGG CAY HGG                                                                258
Gly His Xaa
55

```

## (2) INFORMATION FOR SEQ ID NO: 282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 10..206  
id AAC74428  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 196..257  
id AA074428  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..175



id AA158941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..285  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 165..257  
id AA158941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 37..202  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..166  
id AA148039  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..254  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 156..217  
id AA148039  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 250..285  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 214..249  
id AA148039  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 74..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..207  
id H72224  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 76..153  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq LTCGPALVPRLWA/TC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

AAGAGGCTAG AAGCTGGATT CAGCGTGTCC GCGACCTCAC CTTTAGSTCC TGTGAGGGAC 60

GGCCCGAGGTG GCAGG ATG TCC TGG TCT GGC CTT CTC CAT GGC CTC AAC ACG 111

Met	Ser	Trp	Ser	Gly	Leu	Leu	His	Gly	Leu	Asn	Thr	
-25						-20				-15		
TCC	CTA	ACT	TGT	GGC	CCA	GCT	CTG	GTT	CCC	CGG	CTC	TGG
Ser	Leu	Thr	Cys	Gly	Pro	Ala	Leu	Val	Pro	Arg	Leu	Trp
-10						-5						1
TCC	ATG	GCT	ACC	CTG	AAC	CAG	ATG	CAC	CGC	CTG	GGG	CCC
Ser	Met	Ala	Thr	Leu	Asn	Gln	Met	His	Arg	Leu	Gly	Pro
5						10					15	
CCG	CCT	CGG	AAG	CTG	GGC	CCC	ACG	GAA	GGC	CGG	CCG	CAG
Pro	Pro	Arg	Lys	Leu	Gly	Pro	Thr	Glu	Gly	Arg	Pro	Gln
20						25					30	
GTG	GTC	CTG	TGC	ACG	TTT	ACC	CGC	AAC	CGG			
Val	Val	Leu	Cys	Thr	Phe	Thr	Arg	Asn	Arg			
35						40						

## (2) INFORMATION FOR SEQ ID NO: 283:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..206  
id HSC3CC061  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 94..205  
id H33976  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 1..45  
id AA041823  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 49..93  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 1..45  
 id AA003782  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 25..93  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.1  
 seq LEAFSQAISAIQA/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```

AAKAGCTGCT GTGGCGGCGG CAAC ATG GCG GAC GTG ATA AAT GTC AGT GTG      51
                Met Ala Asp Val Ile Asn Val Ser Val
                        -20                        -15

AAC CTG GAG GCC TTT TCC CAG GCC ATT AGT GCC ATC CAG GCG CTG CGA      99
Asn Leu Glu Ala Phe Ser Gln Ala Ile Ser Ala Ile Gln Ala Leu Arg
                -10                        -5                        1

TCC AGC GTG AGC AGG GTG TTC GAC TGC CTG AAG GAT GGG ATG CGG AAC      147
Ser Ser Val Ser Arg Val Phe Asp Cys Leu Lys Asp Gly Met Arg Asn
                5                        10                        15

AAG GAG ACG CTG GAG GGC CGG GAG AAG GCC TTT ATT GCG CAC TTC CAG      195
Lys Glu Thr Leu Glu Gly Arg Glu Lys Ala Phe Ile Ala His Phe Gln
                20                        25                        30

GAC AAC TTA CAT TCG GTC AAC CGG GAC CCA                                225
Asp Asn Leu His Ser Val Asn Arg Asp Pro
                35                        40

```

## (2) INFORMATION FOR SEQ ID NO: 284:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(210..340)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99

region 172..302  
id AA062591  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 109..204  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.1  
seq RLLSSLLLTMSNN/NP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

AGACCCGATG GACCCCGGCG ACGCSCCATT TTGGAGTCTT CCCTAAGGAT CCTCTACCGG 60
CTTTTCGAGT CAGTGCTGCC GCCGCTGCCC GCGGCTTTGC AGAGCAGG ATG AAT GTG 117
                                         Met Asn Val
                                         -30

ATA GAC CAC GTG CGG GAC ATG GCG GCC GCG GGG CTG CAC TCC AAC GTG 165
Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His Ser Asn Val
      -25                      -20                      -15

CGG CTC CTC AGC AGC TTG TTA CTT ACA ATG AGT AAT AAC AAC CCT GAG 213
Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn Asn Pro Glu
      -10                      -5                      1

TTA TTC TCC CCA CCT CAG AAG TAC CAG CTT TTG GTG TAT CAT GCA GAT 261
Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr His Ala Asp
      5                      10                      15

TCT CTC TTT CAT GAT AAG GAA TAT CGG AAT GCT GTG AGT AAG TAT ACC 309
Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser Lys Tyr Thr
      20                      25                      30                      35

ATG GCT TTA CAG CAG AAG AAA GCG CTA AGT 339
Met Ala Leu Gln Gln Lys Lys Ala Leu Ser
      40                      45

```

## (2) INFORMATION FOR SEQ ID NO: 285:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..41)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90

region 66..105  
id AA085310  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 70..117  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.1  
seq ACLAWTAVRPSAC/CH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```
AAAGTGAGTT TGCGAACGGA GCAGCTGCTG CAGCAGGGCC CATGGCGGAC ACCCAGTACA    60
TCCTGCCCA ATG ACA TCG GCG TGT CTA GCC TGG ACT GCC GTG AGG CCT TCC    111
      Met Thr Ser Ala Cys Leu Ala Trp Thr Ala Val Arg Pro Ser
      -15                      -10                      -5

GCC TGC TGT CAC CCA CAG AGC GCC AAC TGG                                141
Ala Cys Cys His Pro Gln Ser Ala Asn Trp
      1                      5
```

## (2) INFORMATION FOR SEQ ID NO: 286:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(147..290)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 141..284  
id W12393  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 249..289  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..41  
id HSC2TF111  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 60..224

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4

seq VFGMSSSSGASNS/AP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```

ATCTCAACTT GGACTTGCAA TCACAGAACA TTTACCACCA TGAAGAGAA GGAAGTAGN      59
ATG AAT GGA AGT AGG ACT CTA ACG CAC AGC ATT AST GAT GGA CAA CTT      107
Met Asn Gly Ser Arg Thr Leu Thr His Ser Ile Ser Asp Gly Gln Leu
-55              -50              -45              -40

CAA GGT GGC CAG TCC AAT AGT GAA CTA TTT CAG CAG GAG SSA CAG ACA      155
Gln Gly Gly Gln Ser Asn Ser Glu Leu Phe Gln Gln Glu Xaa Gln Thr
              -35              -30              -25

GCA CCA GCT CAA GTT CCT CAA GGC TTT AAT GTT TTT GGA ATG TCC AGT      203
Ala Pro Ala Gln Val Pro Gln Gly Phe Asn Val Phe Gly Met Ser Ser
              -20              -15              -10

TCC TCT GGT GCT TCA AAT TCA GCA CCA CAT CTT GGA TTT CAC TTA GGC      251
Ser Ser Gly Ala Ser Asn Ser Ala Pro His Leu Gly Phe His Leu Gly
              -5              1              5

AGC AAA GSA ACA TCT AGC CTT TCT CAA CAA ACT CCC GGG      290
Ser Lys Gly Thr Ser Ser Leu Ser Gln Gln Thr Pro Gly
10              15              20

```

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(68..194)

(C) IDENTIFICATION METHOD: blastn

```

(D) OTHER INFORMATION: identity 100
                      region 204..330
                      id N35493
                      est

```

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(208..323)

(C) IDENTIFICATION METHOD: blastn

```

(D) OTHER INFORMATION: identity 100
                      region 75..190
                      id N35493

```

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..79)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 318..395  
id N35493  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 186..233  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq FFLFLSFVLMYDG/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

```
ATAAAGAAG CAGCAAATAG AATTCCAC AAAGTAAGTT GACTCTAAAT CTTAAGTATT   60
ACCTAGTTTT TTAAAGGTTT GAATATAATA ATGCAGTATT TGCAGTATAA AAAGGAAGCA  120
ATTGTAGAG AATCATTTTG GTGCTCAAGT CTCTAGCAG TGCCTTATTG CCTCATAGCA  180
AGAAG ATG CTG GGG TTT TTT TTG TTT TTG TCC TTT GTA TTA ATG TAT GAT  230
Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp
   -15               -10               -5

GGT TTG CGC CTT TTT GGC ATT CTT TCA ACA TGT CGT GTA CAT CAC ACC  278
Gly Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr
   1               5               10               15

ATG AAT CAG TTC CTA ATT GAT ATA TCT AGC TTT ACC TCC CGA GTT CGG  326
Met Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Arg
   20               25               30
```

## (2) INFORMATION FOR SEQ ID NO: 288:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 219..380  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 46..207

id N95583  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 213..335  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 46..162  
id AA283710  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 336..380  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 162..206  
id AA283710  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 240..320  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq SIKVLLQSALSLG/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

AGTGGCTCTT CTGACCCAAG GCCCGCCCGT CCAGGTAGGG GGCTGTGGCC TCTAGGGATC   60
AGGGACTACT TACCTGCGAA TCCCGGTTGC CCGCCCGCCA RCACGTCCGK TYCCSTAARG   120
CARAMCGCCT KSGCTCCTGG CTGAACCGTC TTCTCAMCGT TTGSCGGAGT CTGANCTCCC   180
CACGCTTAGT CCACTAACGR AGCTATCCCT GCTCCTGMCC CACAGCTTCT AAGTGCCAG   239
ATG ATG GAG GAG CGT GCC AAC CTG ATG CAC ATG ATG AAA CTC AGC ATC   287
Met Met Glu Glu Arg Ala Asn Leu Met His Met Met Lys Leu Ser Ile
-25                      -20                      -15

AAG GTG TTG CTC CAG TCG GCT CTG AGC CTG GGC CGC AGC CTG GAT GCG   335
Lys Val Leu Leu Gln Ser Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala
-10                      -5                      1                      5

GAC CAT GCC CCC TTG CAG CAG TTC TTT GTA GTG ATG GAG CAC TGC TCA   383
Asp His Ala Pro Leu Gln Gln Phe Phe Val Val Met Glu His Cys Ser
10                      15                      20

```

## (2) INFORMATION FOR SEQ ID NO: 289:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 57..180

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 15..138  
id AA090170  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..286

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 184..244  
id AA090170  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 21..242

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90  
region 1..222  
id HSU46267  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..319

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90  
region 220..396  
id AA048294  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 149..286

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92  
region 139..276  
id AA118611  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..286

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92  
region 88..231  
id AA063937  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 80..130  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq XIVSAALLAFVQT/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```

AGTTGCTCGG GCTGGGGGAT GAGAGCTGCA CCGCGCGGGA YAAGTGGCG GCGGCGCCCG   60
AMGGAGCAGA ACAGAGAGC ATG GAG CTG GAG AAG ATC CTC AGT GCA GCC CTC   112
      Met Glu Leu Glu Xaa Ile Val Ser Ala Ala Leu
      -15                               -10

CTT GCC TTT GTC CAG ACA CAC CTC CCG GAG GCC GAC CTC AGT GGC TTG   160
Leu Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu
      -5                               1                               5                               10

GAT GAG GTC ATC TTC TCC TAT GTG CTK GGG GTC CTG GAG GAC CTG GGC   208
Asp Glu Val Ile Phe Ser Tyr Val Xaa Gly Val Leu Glu Asp Leu Gly
      15                               20                               25

CCC TCG GGC CCA TCA GAG GAG AAC TTC GAT ATC GAG GCT TTC ACT GAG   256
Pro Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu
      30                               35                               40

ATG ATG GAG GCC TAK GTG CCT GGC TTC GCC CAC ATC CCC AGG GGM ACA   304
Met Met Glu Ala Xaa Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr
      45                               50                               55

ATA GGG GAS ATG ATG                                           319
Ile Gly Xaa Met Met
      60
  
```

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 2..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 8..279  
 id T30552  
 est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 3..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 1..271  
                           id C14403  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 2..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 14..285  
                           id T30625  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 4..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 1..270  
                           id T32136  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 3..270  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 1..268  
                           id C14440  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 98..175  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
                           seq SLIPLFXFIGTGA/TG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AGGAAGTCCG TAGTGCTCA TTGCRGATAA TTTTAGCTT AGGGCCTKGT GGCTAGGKCG      60
GTTCTCTCCK KTCCAGTCGG AGACCTCTGC SGVRRRC ATG CTC CGC CAG ATC ATC      115
                               Met Leu Arg Gln Ile Ile
                               -25

GGT CAG GCC AAG AAG CAT CCG AGC TTG ATC CCC CTC TTT KTA TTT ATT      163
Gly Gln Ala Lys Lys His Pro Ser Leu Ile Pro Leu Phe Xaa Phe Ile
-20          -15          -10          -5

GGR ACT GGA GCT ACT GGA GCA ACA CTG TAT CTC TTG CGT CTG GCA TTG      211
Gly Thr Gly Ala Thr Gly Ala Thr Leu Tyr Leu Leu Arg Leu Ala Leu
          1          5          10

TTC AAT CCA GRT GTT TGT TGG GAC AGA RRT AAC CCA GAG CCC TCG AAC      259
Phe Asn Pro Xaa Val Cys Trp Asp Arg Xaa Asn Pro Glu Pro Trp Asn

```

15

20

25

KRA CTG GGC CCC GAA  
 Xaa Leu Gly Pro Glu  
 30

274

## (2) INFORMATION FOR SEQ ID NO: 291:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..332
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
 region 5..137  
 id T78510  
 est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(230..332)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
 region 117..219  
 id R46866  
 est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 37..330
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
 seq WISLTCSLVVVDG/CG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

AAGTGGGTG GAGCCAGGCG TGGAAGTCGA CACAAG ATG GTG AAG GAG ACC CAG	54
Met Val Lys Glu Thr Gln	
-95	
TAC TAT GAC ATC CTG GGC GTG AAG CCC AGC GCG TCC CCG GAG AGA TCA	102
Tyr Tyr Asp Ile Leu Gly Val Lys Pro Ser Ala Ser Pro Glu Arg Ser	
-90 -85 -80	
AGA AGG CCT ATC GGA AGC TGG CGC TCA AGT ACC ACC CGG ACA AGA ACC	150
Arg Arg Pro Ile Gly Ser Trp Arg Ser Ser Thr Thr Arg Thr Arg Thr	
-75 -70 -65	

CGG	ATG	AGG	GCG	AGA	AGT	TTA	AAG	TCA	TAT	CCC	AGG	CAT	ATG	AAG	TGC	198
Arg	Met	Arg	Ala	Arg	Ser	Leu	Asn	Ser	Tyr	Pro	Arg	His	Met	Lys	Cys	
-60					-55					-50					-45	
TTT	CAG	ATC	CAA	AGA	AAA	GGG	ATG	TTT	ATG	ACC	AAG	GCG	GAG	AGC	AGG	246
Phe	Gln	Ile	Gln	Arg	Lys	Gly	Met	Phe	Met	Thr	Lys	Ala	Glu	Ser	Arg	
				-40					-35					-30		
CAA	TBV	AAG	AAG	GAG	GCT	CAG	GCA	CCC	CCA	GCT	TCT	CTT	CAC	CCA	TGG	294
Gln	Xaa	Lys	Lys	Glu	Ala	Gln	Ala	Ala	Pro	Ala	Ser	Leu	His	Pro	Trp	
			-25					-20					-15			
ACA	TCT	TTG	ACA	TGT	TCT	TTG	GTG	GTG	GTG	GAC	GGA	TGC	GGG			336
Thr	Ser	Leu	Thr	Cys	Ser	Leu	Val	Val	Val	Asp	Gly	Cys	Gly			
		-10					-5					1				

TTT CAG ATC CAA AGA AAA GGG ATG TTT ATG ACC AAG GCG GAG AGC AGG 246  
Phe Gln Ile Gln Arg Lys Gly Met Phe Met Thr Lys Ala Glu Ser Arg  
-40 -35 -30

CAA TBV AAG AAG GAG GGT CAG GCA GCC CCA GCT TCT CTT CAC CCA TGG 294  
Gln Xaa Lys Lys Glu Ala Gln Ala Ala Pro Ala Ser Leu His Pro Trp  
-25 -20 -15

ACA TCT TTG ACA TGT TCT TTG GTG GTG GTG GAC GGA TGC GGG 336  
Thr Ser Leu Thr Cys Ser Leu Val Val Val Asp Gly Cys Gly  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 18..194  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 2..178  
id W25476  
est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 359..396  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 347..384  
id W25476  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..278  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 19..276  
id HUM179H07B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 279..379  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 278..378  
id HUM179H07B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 17..175  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 27..185  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 171..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 182..303  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 358..396  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 373..411  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 325..358  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 339..372  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 204..396  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 186..378  
id AA253291  
est

(1X) FEATURE:

[illegible]

(ix) FEATURE:

[illegible]

(1x) FEATURE:

[illegible]

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 59..166  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq RALSTXLFSGIRG/AA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

AGTGGCGAGA CGCAGGGGTC GCGCGCGGGT GAGAGCGTGC GGCCGGATTC ACCACAAC	58
ATG GCA AAT CTT TTT ATA AGG AAA ATG GTG AAC CCT CTG CTC TAT CTC	106
Met Ala Asn Leu Phe Ile Arg Lys Met Val Asn Pro Leu Leu Tyr Leu	
-35 -30 -25	
AGT CGT CAC ACG GTG AAG CCT CGA GCC CTC TCC ACA NTT CTA TTT GGA	154
Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser Thr Xaa Leu Phe Gly	
-20 -15 -10 -5	
TCC ATT CGA GGT GCA GCC CCC GTG GCT GTG GAA CCC GGG GCA GCA GTG	202
Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu Pro Gly Ala Ala Val	
1 5 10	

```

CGC TCA CTT CTC TCA CCC GGC CTC CTG CCC CAT CTG CTG CCT GCG CTG      250
Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His Leu Leu Pro Ala Leu
      15              20              25

GGG TTC AAA AAC AAG ACT GTC CTT AAG AAG CGC TGC AAG GAC TGT TAC      298
Gly Phe Lys Asn Lys Thr Val Leu Lys Lys Arg Cys Lys Asp Cys Tyr
      30              35              40

CTG GTG AAG AGG CGG GGT CGG TGG TAC GTC TAC TGT AAA ACC CAT CCG      346
Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His Pro
      45              50              55              60

AGG CAC AAG CAG AGA CAC ATG TAN ACC CTT TCC CTC CAG AGT CAC GCA      394
Arg His Lys Gln Arg His Met Xaa Thr Leu Ser Leu Gln Ser His Ala
      65              70              75

CAA
Gln
      397

```

## (2) INFORMATION FOR SEQ ID NO: 293:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 115..216
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 41..142  
id H64274  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 74..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..43  
id H64274  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 115..216
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 36..137  
id R16956  
est



## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..33  
id R16956  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 123..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 57..143  
id W04201  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 4..57  
id W04201  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 123..190
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 50..117  
id N76590  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 2..43  
id N76590  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(107..195)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 323..411  
id N70265  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 106..201
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq RIHLQQRSPGSQG/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```

ACCCTGCCTC ATGCACCTTA TGGGTAGGTT TTTAGGGTCC GCGGTTGGTC AKACCGGAGC   60
ACTTGGCCTG AAGACCTGGA ATTGGYGACT TCGATATTAA CAAGG ATG GCG GCG GCC   117
                                     Met Ala Ala Ala
                                     -30

GCA GCA AGT CGA GGA KTC GGG GCA AAG CTG GGC CTG CGT GAN ATT CGC   165
Ala Ala Ser Arg Gly Xaa Gly Ala Lys Leu Gly Leu Arg Xaa Ile Arg
      -25                      -20                      -15

ATC CAC TTA TGT CAG CGC TCG GCG GGC AGC CAG GGC GTC AGG GAC TTC   213
Ile His Leu Cys Gln Arg Ser Pro Gly Ser Gln Gly Val Arg Asp Phe
      -10                      -5                      1

ATT                                     216
Ile
  5

```

## (2) INFORMATION FOR SEQ ID NO: 294:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..279)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..279  
id M85423  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(196..289)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 466..559  
id AA126476  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(133..194)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 560..621  
id AA126476  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(105..137)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 616..648  
id AA126476  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 152..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..141  
id R33928  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 160..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 14..146  
id H67425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 161..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..132  
id W04820  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 101..232  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq IALTLPMSLSRA/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

```
AACTTCTTCA TCTTGGTGGT CCTTGCCCAG TTATTTTGCC TCATTAGACA TCAAGAAATG   60
GAGAAAGACT GAAAGTTAAT ATCTTAAGTG CTTGTTCTTC ATG TTT CCT TCT TGT   115
                               Met Phe Pro Ser Cys
                               -40
TAT TTA TGC TAT TCT CTT TGT GGC TCC ATT CTT CTT TCA ATC TTC TCA   163
Tyr Leu Cys Tyr Ser Leu Cys Gly Ser Ile Leu Leu Ser Ile Phe Ser
-35                               -25
GCT TAT AAC CGT CTT TCC CTT ATG CTA AGG ATA GCC CTT ACA CTC ATC   211
```

Ala Tyr Asn Arg Leu Ser Leu Met Leu Arg Ile Ala Leu Thr Leu Ile  
-20 -15 -10

CCA TCT ATG CTG TCA AGG CCT GCT GGT TGG TGC TGG TAC AAG GAG CCC 259  
Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys Glu Pro  
-5 1 5

ACT CAG CAG TTT TCT TAC CTT TGC CTG CCC TGC GGG 295  
Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys Gly  
10 15 20

## (2) INFORMATION FOR SEQ ID NO: 295:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 36..345  
id R32875  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(52..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 35..301  
id N69845  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..52)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 302..345  
id N69845  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(39..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 46..325  
id H20723

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(30..318)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 35..323  
 id HSC3JH072  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(65..318)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 43..296  
 id R02144  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 125..304  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq QLXFLYFVCCIFQ/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

```

AAMAAGCTCC CAGCCTCCAG AGGCTCTCAA TGAAGAGTCA CCTTCATGGT CGTCTYCAGG    60
AACAGGACGG ATGAMGAAGG GGTGGGGTTA AGACTCAGGG GCACCTGAGG GTCTGAGCCC    120
CCTT ATG AGT ACC CAA GAM GGA CTG TCT ATG CAT GCA CAC CCA CAA GCC    169
Met Ser Thr Gln Xaa Gly Leu Ser Met His Ala His Pro Gln Ala
-60                      -55                      -50

TAT ACA CCA TTT ATA TAC CTA CAC GCA CGC AAG AGA CGC GGA GAG ATA    217
Tyr Thr Pro Phe Ile Tyr Leu His Ala Arg Lys Arg Arg Gly Glu Ile
-45                      -40                      -35                      -30

GGC GAT GCA GAC TCG CGA TTC AAT GAT CGA TAT GCT CAT AAR AGT GCT    265
Gly Asp Ala Asp Ser Arg Phe Asn Asp Arg Tyr Ala His Lys Ser Ala
-25                      -20                      -15

CAA TTA TMT TTT CTG TAT TTT GTA TGC TGT ATT TTC CAA GAC GTA TAT    313
Gln Leu Xaa Phe Leu Tyr Phe Val Cys Cys Ile Phe Gln Asp Val Tyr
-10                      -5                      1

TAT KTN    319
Tyr Xaa
5

```

## (2) INFORMATION FOR SEQ ID NO: 296:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs  
 (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..170)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 118..287  
id AA035134  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..170)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 116..285  
id N54275  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..170)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 119..288  
id AA088715  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(19..170)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 115..266  
id N78023  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(12..133)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 157..278  
id AA100730  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(127..170)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 119..162  
id AA100730

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 56..118
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq SSCSCSLISFTRG/DK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

```
ATCTTAGTGC CTTTATCTGT CTTTATGTCT TGGGGTTGGG GTAGGTAGAT ACCAA ATG      58
                                         Met
AAA CAC TTT CAG GAC CTT CCT TCC TCT TGC AGT TGT TCT TTA ATC TCC      105
Lys His Phe Gln Asp Leu Pro Ser Ser Cys Ser Cys Ser Leu Ile Ser
-20                      -15                      -10                      -5
TTT ACT AGA GGA GAT AAA TAT TTT GCA TAT AAT GAA GAA ATT TTT CTA      154
Phe Thr Arg Gly Asp Lys Tyr Phe Ala Tyr Asn Glu Glu Ile Phe Leu
                      1                      5                      10
GTA TAT AAC GCA GAC CAG                                          172
Val Tyr Asn Ala Asp Gln
                      15
```

## (2) INFORMATION FOR SEQ ID NO: 297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(29..369)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 103..443  
id W26961  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(383..424)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 48..89  
id W26961  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(34..369)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 100..435  
id W26018  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(383..424)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 45..86  
id W26018  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(200..369)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 111..230  
id W26871  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(143..200)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 281..338  
id W26871  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(383..424)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 56..97  
id W26871  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(94..123)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 361..390  
id W26871  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(119..369)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 104..354  
id W26098



est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(383..424)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 49..90  
 id W26098  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 31..302  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 1..272  
 id N99777  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 302..369  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 273..340  
 id N99777  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 155..340  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq SILGIISVPLSIG/YC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```

AGTGAAAAGA AGATGCCTAG AGAATGGCAA TTTAAAAGAA AAAGATATAC TTGTTTTGCC   60
CCTTGAAECTG ACCGACACTG GTTCCCATGA AGCGGCTACC AAAGCTGTTC TCCAGGAGTT   120
TGGTAGAATC GACATTCIGG TCAACAATGG TGGA ATG TCC CAG CGT TCT CTG TGC   175
                               Met Ser Gln Arg Ser Leu Cys
                               -60

ATG GAT ACC AGC TTG GAT GTC TAC AGA RAG CTA ATA GAG CTT AAC TAC   223
Met Asp Thr Ser Leu Asp Val Tyr Arg Xaa Leu Ile Glu Leu Asn Tyr
-55                               -50                               -45                               -40

TTA GGG ACG GTG TCC TTG ACA AAA TGT GTT CTG CCT CAC ATG ATC GAG   271
Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile Glu
-35                               -30                               -25

AGG AAG CAN KKA AAG ATT GTT ACT GTG AAT AGC ATC CTG GGT ATC ATA   319
Arg Lys Xaa Xaa Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile Ile
-20                               -15                               -10

TCT GTA CCT CTT TCC ATT GGA TAC TGT GCT AGC RAG CAT GCT CTS HGG   367
Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Xaa His Ala Leu Xaa

```

-5

1

5

GGT TTT TTT AAT RDH CTT CGA ACA SAD CTT GCC ACA TAC CCA GGT ATA 415  
Gly Phe Phe Asn Xaa Leu Arg Thr Xaa Leu Ala Thr Tyr Pro Gly Ile  
10 15 20 25  
ATA GTT TCT 424  
Ile Val Ser

## (2) INFORMATION FOR SEQ ID NO: 298:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 179..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 160..329  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 83..164  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 383..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 366..420  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..66
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..46  
id AA159241  
est

WO 99/06550

326

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..383
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 324..365  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..102
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 47..83  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..215
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 81..193  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 216..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 195..308  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..102
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..31  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 390..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 374..421  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 324..349  
id AA076222

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 241..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 202..404  
id AA149750  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 40..215  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..176  
id AA149750  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 241..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 181..383  
id W63593  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 63..184  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 3..124  
id W63593  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 179..243  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 120..184  
id W63593  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 320..438  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 267..385  
id AA130386  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 216..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98

region 164..276  
id AA130386  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 103..215  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 50..162  
id AA130386  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 82..375  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq LALRTSWISSVCS/VT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```

AAGTGACGCG GCCCAAGGGC GGAAGTGAGA AAGTTGTCTG CGTCTCGAGG CGAGTTGGCG      60
GACTGTGCGC GCGGCGGGGC G ATG GGG GGC TCG GGC AGT CGC CTG TCC AAG      111
                        Met Gly Gly Ser Gly Ser Arg Leu Ser Lys
                        -95                               -90

GAG CTG CTG GCC GAR TAC CAG GAC TTG ACG TTC CTG ACG AAG CAG GAG      159
Glu Leu Leu Ala Glu Tyr Gln Asp Leu Thr Phe Leu Thr Lys Gln Glu
                        -85                               -75

ATC CTC CTA GCC CAC AGG CGG TTT TGT GAG CTG CTT CCC CAG GAG CAG      207
Ile Leu Leu Ala His Arg Arg Phe Cys Glu Leu Leu Pro Gln Glu Gln
                        -70                               -60

CGG ASK NGG AGT CCT CAC TTC GGG CAC AAG TGC CCT TCG AGC AGA TTC      255
Arg Xaa Xaa Ser Arg His Phe Gly His Lys Cys Pro Ser Ser Arg Phe
                        -55                               -45

TCA GCE TTC CAG AGC TCA AGG CCA ACC CCT TCA AGG AGC GAA TCT GCA      303
Ser Ala Phe Gln Ser Ser Arg Pro Thr Pro Ser Arg Ser Glu Ser Ala
                        -40                               -25

GGG TCT TCT CCA CAT CCC CAG CCA AAG ACA GCC TTA GCT TTG AGG ACT      351
Gly Ser Ser Pro His Pro Gln Pro Lys Thr Ala Leu Ala Leu Arg Thr
                        -20                               -10

TCC TGG ATC TCC TCA GTG TGT TCA GTG ACA CAG CCA CGC CAG ACA TCA      399
Ser Trp Ile Ser Ser Val Cys Ser Val Thr Gln Pro Arg Gln Thr Ser
                        -5                               1                               5

AGT CCC ATT ATG CCT TCC SCA TCT TTG ACT TTG ATG ATG ACG      441
Ser Pro Ile Met Pro Ser Ala Ser Leu Thr Leu Met Met Thr
                        10                               15                               20

```

## (2) INFORMATION FOR SEQ ID NO: 299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 9..169  
id N76992  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 162..280
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 168..286  
id N76992  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 8..119  
id W39234  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..280
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 176..283  
id W39234  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 118..167  
id W39234  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..160
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..141  
id R06371  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 173..260  
id R06371  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 159..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 138..174  
id R06371  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 20..159  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..140  
id R06399  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 161..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 141..260  
id R06399  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..139  
id AA043154  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 166..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 141..255  
id AA043154  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 132..215  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
 seq PLSDSWALLPASA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

AACAACTTCC GGCCCCACTG AGCGGTGTCC TGACCCGATT ACAGCTAGGT AGTGGAGCGC    60
CGCTGCTTAC CTGGGTGCAG GACACAGCCG GAGTGGCTGG GGGAGCTCCG CCGCGCCGGA    120
CGCCCGTGAC C ATG TGG AGG CTG CTG GCT GCG GCT AGT GCG CCG CTC CTG    170
           Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu
                   -25                               -20

CGG GTG CCC TTG TCA GAT TCC TGG GCA CTC CTC CCC GCC AGT GCT GGC    218
Arg Val Pro Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly
-15                   -10                               -5                               1

GTA AAG ACA CTG CTC CCA GTA CCA AGT TTT GAA GAT GTT TCC ATT CCT    266
Val Lys Thr Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro
           5                   10                               15

GAA AAA CCC AAG CTA CTG    284
Glu Lys Pro Lys Leu Leu
           20
  
```

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 169..332  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 163..326  
 id H71676  
 est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 92..170  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
 region 87..165  
 id H71676  
 est



## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 20..85  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 18..83  
                           id H71676  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 334..364  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 330..360  
                           id H71676  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 264..376  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 3..115  
                           id AA020192  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 6..347  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
                           seq ATFVTQALIQXYA/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

```

AAAAA ATG GCG GAT CAT GTG CAG AGC CTG GCC CAA CTA GAG AAT CTG TGC   50
      Met Ala Asp His Val Gln Ser Leu Ala Gln Leu Glu Asn Leu Cys
                -110                      -105                      -100

AAA CAG CTG TAT GAA ACC ACA GAC ACA RSC AST CGG AGC TCC SAG GCA   98
Lys Gln Leu Tyr Glu Thr Thr Asp Thr Xaa Xaa Arg Ser Ser Xaa Ala
      -95                      -90                      -85

GAG AAA GCS TTG GTT GAR TTT ACC AAC AGC CCT GAT TGC CTG AGC AAG   146
Glu Lys Ala Leu Val Glu Phe Thr Asn Ser Pro Asp Cys Leu Ser Lys
      -80                      -75                      -70

TGC CAG CTA CTC CTC GAA AGA GGA AGT TCC TCT TAC TCC CAG TTA CTG   194
Cys Gln Leu Leu Leu Glu Arg Gly Ser Ser Ser Tyr Ser Gln Leu Leu
      -65                      -60                      -55

GCA GCT ACA TGC CIT ACC AAG CTT GTA TCA CGC ACA AAC AAC CCC CTA   242
Ala Ala Thr Cys Leu Thr Lys Leu Val Ser Arg Thr Asn Asn Pro Leu
      -50                      -45                      -40

CCA TTG GAA CAG CGA ATA GAT ATT CGG AAC TAT GTG CTC AAC TAS CTT   290
Pro Leu Glu Gln Arg Ile Asp Ile Arg Asn Tyr Val Leu Asn Xaa Leu
      -35                      -30                      -25                      -20

```

GCC ACT CGG CCG AAG TGG GGT ACT TTC GTG ACA CAA GCA CTT ATT CAG 338  
Ala Thr Arg Pro Lys Leu Ala Thr Phe Val Thr Gln Ala Leu Ile Gln  
-15 -10 -5

TKA TAT GCC AGA ATC ACA AAA CTG GGC TGG TTT GAC 374  
Xaa Tyr Ala Arg Ile Thr Lys Leu Gly Trp Phe Asp  
1 5

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..222  
id H39781  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..158  
id AA017398  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 172..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 159..222  
id AA017398  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..220  
id AA059110  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 17..235  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 1..219  
                           id AA037143  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 56..235  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 56..235  
                           id R75754  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 14..55  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 15..56  
                           id R75754  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 62..226  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
                           seq TCSVCCYLFWLIA/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

```

AACACTTCCT GGTGGATCCG AGTGAGGCCA CGGGGTAGGG GTTGGCGCTC AGGCGGCGAC   60
C ATG GCG TAT CAC GGC CTC ACT GTG CCT CTC ATT GTG ATG AGC GTG TTC   109
  Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe
  -55 -                -50                -45                -40

TGG GGC TTC GTC GGC TTC TTG GTG CCT TGG TTC ATC CCT AAG GGT CCT   157
Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro
          -35                -30                -25

AAC CGG GGA GTT ATC ATT ACC ATG TTG GTG ACC TGT TCA GTT TGC TGC   205
Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys
          -20                -15                -10

TAT CTC TTT TGG CTG ATT GCA ATT CCG GCC TGG   238
Tyr Leu Phe Trp Leu Ile Ala Ile Pro Ala Trp
          -5                1

```

## (2) INFORMATION FOR SEQ ID NO: 302:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs

(B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(71) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

(1x) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(397..432)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 283..318  
                           id H83411  
                           est

(1x) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 54..227  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
                           seq GGILMGSFQGTIA/GQ

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

ATATTTGCCC CTTACTTTAT CTTGTGCCTT GAGAAATTGC TGGGGAGAGA GGT ATG	56
Met	
TCC ACT GGG CAG CTG TAC AGG ATG GAG GAT ATA GGG CGT TTC CAC TCC	104
Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His Ser	
-55 -50 -45	
CAG CAG CCA GGT TCC CTC ACC CCA AGC TCA CCC ACT GTT GGG GAG ATT	152
Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu Ile	
-40 -35 -30	
ATC TAC AAT AAC ACC AGA AAC ACA TTG GGG TGG ATT GGG GGT ATC CTT	200
Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile Leu	
-25 -20 -15 -10	
ATG GGT TCT TTT CAG GGA ACC ATT GCT GGA CAA GGC ACA GGA GCC ACC	248
Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala Thr	
-5 1 5	
TCC ATT TCT GAG CTC TGC AAG GGA CAA GAA CTA GAG CCA TCA GGG GCT	296
Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly Ala	
10 15 20	
GGG CTC ACT GTG GCC CCA CCC CAA GCC GTC AGC CTC CAS GGA TCA CAC	344
Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ser His	
25 30 35	
CCT GCC TTG GCT GCT ACA GCT TTT TCA CTC CAS TGC CCT AGG GGA GTT	392
Pro Ala Leu Ala Ala Thr Ala Phe Ser Leu Xaa Cys Pro Arg Gly Val	
40 45 50 55	
CAG CAS CTA ATG ATC TCT ATC TCT GAA CAT CTC TTC ATC CAT GCT	437

Gln Xaa Leu Met Ile Ser Ile Ser Glu His Leu Phe Ile His Ala  
60 65 70

## (2) INFORMATION FOR SEQ ID NO: 303:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (11) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..321  
id T31485  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..311  
id HSC38B061  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..325
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 70..260  
id T66273  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 69..140
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 5..76  
id T66273  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 6..224

id R24829  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 236..275  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 243..282  
id R24829  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 50..318  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 10..278  
id HSC2LF071  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 282..332  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq RWWCFHLQAEASA/HP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

```

ATAATAATAT CTAAAAAGCT AAATTTTAAA TACCAGCTTT ACATAAATGA TTGTKGACTC   60
TGGTCTGTGT CTGACACCTT TCCAGAAAAA AGTCAATTGT TCAGGTACAC CAAAGAGGAA   120
GAAGAGCTGT GGAGGCCACC CTCTACAAAG CTTTATAGAA CTTCTGGATC TAACTCACAA   180
ACAAGCTTCC AGAAGAGACT AGAGACCTTA GGCCAGSAGA TGAAGGAGTT CAGTAGCAAA   240
GTCACACCTG TCCAATTCCC TGAGCTTTGC TCACTCAGCT A ATG GSA TGG CAA AGG   296
                                     Met Gly Trp Gln Arg
                                     -15

TGG TGG TGC TTT CAT CTT CAG GCA GAA GCC TCT GCC CAT CCC CCT CAA   344
Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser Ala His Pro Pro Gln
    -10                -5                1

GGG CTG CAG   353
Gly Leu Gln
    5

```

## (2) INFORMATION FOR SEQ ID NO: 304:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 80..236

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 34..190  
id N34164  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 91..257

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 66..232  
id R89543  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 91..254

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 66..229  
id H59647  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 126..170

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5  
seq VIFFACVVRVRDG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGGTGACCTG GGCCGAGCCC TCCCGGTCCG CTAAGATTGC TGAGGAGCCG GCGGSTAGCT 60

GGCAGGCGCC GACTTCCGAA GGCCGCCGTC CGGGCGAGGT GTCCTCATGA CTTCTCTTGT 120

GGACC ATG TCC GTG ATC TTT TTT GCC TGC GTG GTA CGG GTA AGG GAT GGA 170

Met Ser Val Ile Phe Phe Ala Cys Val Val Arg Val Arg Asp Gly  
-15 -10 -5

CTG CCC CTC TCA GCC TCT ACT GAT TTT TAC CAC ACC CAA GAT TTT TTG 218

Leu Pro Leu Ser Ala Ser Thr Asp Phe Tyr His Thr Gln Asp Phe Leu  
5 10 15

GAA TGG AGG AGA CGG CTC AAG AGT TTA GCC TTG CGA CTG AAG 260

Glu Trp Arg Arg Arg Leu Lys Ser Leu Ala Leu Arg Leu Lys  
20 25 30

## (2) INFORMATION FOR SEQ ID NO: 305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..210
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 29..195  
id R88607  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 16..134  
id AA035300  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 134..242  
id AA035300  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..207  
id AA147873  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(128..244)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 263..379  
id AA147836  
est

## (ix) FEATURE:

- (A) NAME/KEY: other



(B) LOCATION: complement(38..131)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 375..468  
                           id AA147336  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 136..244  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 91..199  
                           id T69348  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 45..138  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..94  
                           id T69348  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 66..113  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
                           seq TALAAXTWLGWVG/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```

AATTAGCGCG TAACGCASAG ACTGCTTGCT GCGGCAGAGA CGCCAGAKST GCAGCTCCAG      60
CAGCA ATG GCA GTG ACG GCG TTG GCG GCG MRG ACG TGG CTT GGC GTG TGG      110
  Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp
    -15              -10              -5

GGC GTG AGG ACC ATG CAA GCC CGA GGC TTC GGC TCG GAT CAG TCC GAG      158
Gly Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu
   1              5              10              15

AAT GTC GAC CGG GGC GCG GGC TCC ATC CGG GAA GCC GGT GGG GCC TTC      206
Asn Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe
    20              25              30

GGA AAS AGA GAG CAG GCT GAA GAS SAA CGA TAT TTC                        242
Gly Xaa Arg Glu Gln Ala Glu Xaa Xaa Arg Tyr Phe
    35              40

```

## (2) INFORMATION FOR SEQ ID NO: 306:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 151..402

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 100.0  
region 1..252  
id HSU21129  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 155..402

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 99.6  
region 1..248  
id HSU18728  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 131..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..272  
id H27256  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 161..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 31..272  
id W95921  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 296..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 141..247  
id C17793  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 151..252

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..102  
id C17793  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 174..402  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..229  
                           id AA180902  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 199..402  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 1..204  
                           id R58323  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 235..288  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 12  
                           seq FTLFLALIGGTSG/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```

ACATGCCACA CCACAAGATC CCCACAATGA CATAACTCCA TTCAGAGACT GCGGTGACTG   60
GGCTGGGTCT CCCCACCCCC CCCTTCAGCT CTTGTATCAC TCAGAATCTG GCAGCCAGTT  120
CCGTCCTGAC AGAGTTCACA GCATATATTG GTGGATTCTT GTCCATAGTG CATCTGCTTT  180
AAGAATTAAc GAAAGCAGTG TCAAGACAGT AAGGATTCAA ACCATTTGCC AAAA ATG   237
                                     Met
AGT CTA AGT GCA TTT ACT CTC TTC CTG GCA TTG ATT GGT GGT ACC AGT   285
Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr Ser
   -15                      -10                      -5
GGC CAG TAC TAT GAT TAT GAT TTT CCC CTA TCA ATT TAT GGG CAA TCA   333
Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln Ser
   1                      5                      10                      15
TCA CCA AAC TGT GCA CCA GAA TGT AAC TGC CCT GAA AGC TAC CCA AGT   381
Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro Ser
          20                      25                      30
GCC ATG TAC TGT GAT GAG CTG   402
Ala Met Tyr Cys Asp Glu Leu
          35

```

## (2) INFORMATION FOR SEQ ID NO: 307:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs  
 (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 120..272  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 96.1  
region 1..151  
id HSU21128  
vrt

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..272  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 96.0  
region 1..147  
id HSU18728  
vrt

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 141..272  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 40..171  
id H27256  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 100..136  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..37  
id H27256  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 141..272  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 40..171  
id W95921  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 141..245  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 52..156  
id AA093526

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 89..136  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 2..49  
                           id AA093526  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 145..272  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 1..128  
                           id AA180902  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 141..223  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 20..102  
                           id C17793  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 206..259  
 (C) IDENTIFICATION METHOD: Von Heljne matrix  
 (D) OTHER INFORMATION: score 12  
                           seq FTLFLALIGGTSG/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```

ATAACGCCAT TCAGAGACTG GCGTGACTGG GCTGGGTCTC CCCACCCCCC CCTTCAGGTC   60
TTGTATGACT CAGAATCTGG CAGCCAGTTC CGTCCTGACA GAGTTCACAG CATATATTGG   120
TSGATTCTTG TCCAWAAGTG GVATCTGCTT TARGAWTTAA CGAAAGCAGT GTCAAGACAG   180
TAAGGATTCA AACCATTTCG CAAAA ATG AGT CTA AGT GCA TTT ACT CTC TTC   232
                        Met Ser Leu Ser Ala Phe Thr Leu Phe
                        -15                               -10

CTG GCA TTG ATT GGT GGT ACC AGT GGC CAG TAC TAT GAT TGG   274
Leu Ala Leu Ile Gly Gly Thr Ser Gly Gln Tyr Tyr Asp Trp
      -5                               1                               5

```

## (2) INFORMATION FOR SEQ ID NO: 308:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 65..433

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 100.0  
region 1..369  
id HSU21128  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 69..433

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 99.7  
region 1..365  
id HSU18728  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 45..433

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 1..389  
id H27256  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 75..433

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 31..389  
id W95921  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 210..433

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 141..364  
id C17793  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 65..166

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..102  
id C17793  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 88..433  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..346  
 id AA180902  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 113..370  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 1..258  
 id R58323  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 149..202  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 12  
 seq FTLFLALIGGTSG/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

```

AGCTCTTGTA TCACTCAGAA TCTGGCAGCC AGTTCCTGCC TGACAGAGTT CACAGCATAT      60
ATTGGTGGAT TCTTGTCAT AGTGCATCTG CTTTAAGAAT TAACGAAAGC AGTGTCAAGA     120
CAGTAAGGAT TCAAACCATT TGCCAAAA ATG AGT CTA AGT GCA TTT ACT CTC         172
                               Met Ser Leu Ser Ala Phe Thr Leu
                               -15

TTC CTG GCA TTG ATT GGT GGT ACC AGT GCC CAG TAC TAT GAT TAT GAT       220
Phe Leu Ala Leu Ile Gly Gly Thr Ser Gly Gln Tyr Tyr Asp Tyr Asp
-10                               -5                               1                               5

TTT CCC CTA TCA ATT TAT GGG CAA TCA TCA CCA AAC TGT GCA CCA GAA       268
Phe Pro Leu Ser Ile Tyr Gly Gln Ser Ser Pro Asn Cys Ala Pro Glu
                               10                               15                               20

TGT AAC TGC CCT GAA AGC TAC CCA AGT GCC ATG TAC TGT GAT GAG CTG       316
Cys Asn Cys Pro Glu Ser Tyr Pro Ser Ala Met Tyr Cys Asp Glu Leu
                               25                               30                               35

AAA TTC AAA AGT GTA CCA ATG GTG CCT CCT GGA ATC AAG TAT CTT TAC       364
Lys Leu Lys Ser Val Pro Met Val Pro Pro Gly Ile Lys Tyr Leu Tyr
                               40                               45                               50

CTT AGG AAT AAC CAG ATT GAC CAT ATT GAT GAA AAG GCC TTT GAG AAT       412
Leu Arg Asn Asn Gln Ile Asp His Ile Asp Glu Lys Ala Phe Glu Asn
                               55                               60                               65                               70

GTA ACT GAT CTG CAG TGG CTC GGG                                         436
Val Thr Asp Leu Gln Trp Leu Gly
                               75

```

(2) INFORMATION FOR SEQ ID NO: 309:

## (2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(v1) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 75..345  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 96.3  
region 1..269  
id HUMD3A07M5  
vrt

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 91..150  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq LLLLLLFFLLYMA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

AATTTGAATT GGGGCGTGTC TAGAAAGAGA AGCCATAGTC GGCGAGCAAC GCTGGAGCAT	60
CCCGCTCTGG TGCCGCTGCA GCCGGCAGAG ATG GTT GAG CTC ATG TTC CCG CTG	114
Met Val Glu Leu Met Phe Pro Leu	
-20 -15	
TTG CTC CTC CTT CTG CCC TTC CTT CTG TAT ATG GCT GCG CCC CAA ATC	162
Leu Leu Leu Leu Leu Pro Phe Leu Leu Tyr Met Ala Ala Pro Gln Ile	
-10 -5 1	
AGG AAA ATG CTG TCC AGT GGG GTG TGT ACA TCA ACT GTT CAG CTT CCT	210
Arg Lys Met Leu Ser Ser Gly Val Cys Thr Ser Thr Val Gln Leu Pro	
5 10 15 20	
GGG AAA GTA GTT GTG GTC ACA GGA GGT AAT ACA GGT ATC GGG AAG GAG	258
Gly Lys Val Val Val Thr Gly Ala Asn Thr Gly Ile Gly Lys Glu	
25 30 35	



```

ACA GCC AAA GAG CTG GCT CAG AGA GGA GCT CGA GTA TAT KTA GGT TNN      306
Thr Ala Lys Glu Leu Ala Gln Arg Gly Ala Arg Val Tyr Xaa Ala Xaa
      40                      45                      50

NGG GAT GTG GAA AAG GGG GAA TTG GTG GCC ARA GAG ATC CAG ACC ACC      354
Xaa Asp Val Glu Lys Gly Glu Leu Val Ala Xaa Glu Ile Gln Thr Thr
      55                      60                      65

ACA GGG AAN SAG CAG GTG TTG GTG CGG RAA CTG GAC CTG TCT GAT ACT      402
Thr Gly Xaa Xaa Gln Val Leu Val Arg Xaa Leu Asp Leu Ser Asp Thr
      70                      75                      80

AAG TCT ATT CGA GGT TTT GCT                                          423
Lys Ser Ile Arg Ala Phe Ala
      85                      90

```

## (2) INFORMATION FOR SEQ ID NO: 310:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..303
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96  
region 1..171  
id HSC1R  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..303
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98  
region 24..183  
id HUMC1R  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 181..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 1..123  
id T74375  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 170..213  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 1..44  
id T64778  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 184..228  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.1  
seq LLYLLVPALEFCRA/GG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```
AAAAACTCAG ATCTTTTGT TATGCAAATA GTTCATICCC TCCAACATTC CTCCGGGAAT   60
GGTCCCCCCT CCACTCCACA GAAAACCCCTC CCCTCCCTGC TGTGCATGAC GCGGGCTCCC   120
TCTGSACACA GKGVMCRAAG ACGCTGTGGG GAKAGCCCCA GGATTCAACA CGGGCCTTGA   180
GAA ATG TGG CTC TTG TAC CTC CTG GTG CCG GCC CTG TTC TGC AGG GCA   228
  Met Trp Leu Leu Tyr Leu Leu Val Pro Ala Leu Phe Cys Arg Ala
   -15                      -10                      -5

GGA GGC TCC ATT CCC ATC CCT CAG AAG TTA TTT GGG GAG GTG ACT TCC   276
Gly Gly Ser Ile Pro Ile Pro Gln Lys Leu Phe Gly Glu Val Thr Ser
   1                      5                      10                      15

CCT CTG TTC CCC AAG CCT TAC CCC AAC GGG   306
Pro Leu Phe Pro Lys Pro Tyr Pro Asn Gly
   20                      25
```

## (2) INFORMATION FOR SEQ ID NO: 311:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 50..263  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 99  
region 1..214  
id HSSPG28  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..263
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 99  
region 1..189  
id HSCRISP3G  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 51..146
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7  
seq LLFLVAGLLPSFP/AN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```

AATATATACG GCTCTAACCT TCTCTCTCTC CACCTTCCTT CTGTCAATAG ATG AAA      56
                                         Met Lys

CAA ATA CTT CAT CCT GCT CTG GAA ACC ACT GCA ATG ACA TTA TTC CCA      104
Gln Ile Leu His Pro Ala Leu Glu Thr Thr Ala Met Thr Leu Phe Pro
-30          -25          -20          -15

GTG CTG TTG TTC CTG GTT GCT GGG CTG CTT CCA TCT TTT CCA GCA AAT      152
Val Leu Leu Phe Leu Val Ala Gly Leu Leu Pro Ser Phe Pro Ala Asn
          -10          -5          1

GAA GAT AAG GAT CCC GCT TTT ACT GCT TTG TTA ACC ACC CAA ACA CAA      200
Glu Asp Lys Asp Pro Ala Phe Thr Ala Leu Leu Thr Thr Gln Thr Gln
          5          10          15

GTG CAA AGG GAG ATT GTG AAT AAG CAC AAT GAA CTG AGG AGA GCA GTA      248
Val Gln Arg Glu Ile Val Asn Lys His Asn Glu Leu Arg Arg Ala Val
          20          25          30

TCT CCC CCT GCC AAA      263
Ser Pro Pro Ala Lys
          35

```

## (2) INFORMATION FOR SEQ ID NO: 312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..147

(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 97  
region 1..335  
id HSU03877  
vrt

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 213..467  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 232..486  
id AA150097  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 35..204  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 55..224  
id AA150097  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 43..467  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 56..480  
id AA155808  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 43..404  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 73..434  
id AA147966  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 395..467  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 424..496  
id AA147966  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 51..467  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..417  
id AA058479  
est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 70..405  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 1..336  
 id W46890  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 394..425  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 326..357  
 id W46890  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 52..102  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.9  
 seq LFLTMLTLALVKS/QD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```

AACTCCCCCTC GCTGCCCGGG CCCGGAGCGC ASSNGGCCGC ACAGATTCAC A ATG TTG      57
                                     Met Leu

AAA GCC CTT TTC CTA ACT ATG CTG ACT CTG GCG CTG GTC AAG TCA CAG      105
Lys Ala Leu Phe Leu Thr Met Leu Thr Leu Ala Leu Val Lys Ser Gln
-15                               -10                               -5                               1

GAC ACC GAA GAA ACC ATC ACG TAC ACG CAA TGC ACT GAC GGA TAT GAG      153
Asp Thr Glu Glu Thr Ile Thr Tyr Thr Gln Cys Thr Asp Gly Tyr Glu
                    5                               10                               15

TGG GAT CCT GTG AGA CAG CAA TGC AAA GAT ATT GAT GAA TGT GAC ATT      201
Trp Asp Pro Val Arg Gln Gln Cys Lys Asp Ile Asp Glu Cys Asp Ile
                20                               25                               30

GTC CCA GAC GCT TGT AAA GGT GGA ATG AAG TGT GTC AAC CAC TAT GGA      249
Val Pro Asp Ala Cys Lys Gly Met Lys Cys Val Asn His Tyr Gly
                35                               40                               45

GGA TAC CTC TGC CTT CCG AAA ACA GCC CAG ATT ATT GTC AAT AAT GAA      297
Gly Tyr Leu Cys Leu Pro Lys Thr Ala Gln Ile Ile Val Asn Asn Glu
                50                               55                               60                               65

CAG CCT CAG CAG GAA ACA CAA CCA GCA GAA GGA ACC TCA GGG GCA ACC      345
Gln Pro Gln Gln Glu Thr Gln Pro Ala Glu Gly Thr Ser Gly Ala Thr
                    70                               75                               80

ACC GGG GTT GTA GCT GCC DNC AGC ATG GCA ACC AGT GBA GTG TTG MNN      393
Thr Gly Val Val Ala Ala Xaa Ser Met Ala Thr Ser Xaa Val Leu Xaa
                    85                               90                               95

GGG GGT GGT TTT GTG GCC ACT GCT GCT GCA GTC GCA GGC CCT GAA ATG      441
Gly Gly Gly Phe Val Ala Ser Ala Ala Ala Val Ala Gly Pro Gln Met
                100                               105                               110

```

CAG ACT GGC CGG AAT AAC TTI GTC  
Gln Thr Gly Arg Asn Asn Phe Val  
115 120

465

## (2) INFORMATION FOR SEQ ID NO: 313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96  
region 1..204  
id HUMTCAYV  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 93  
region 1..207  
id MACTCRAAQ  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 94  
region 1..204  
id MACTCRAAR  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 50..115
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq LLILWFHLCVSS/IL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AATTTTGGCT GCAAAACGTT TTTCTGCTGT GGGTACGTGA GCAGGAAAC ATG GAG AAG 58  
Met Glu Lys  
-20

```

AAT CCT TTC GCA GCC CCA TTA CTA ATC CTC TGG TTT CAT CTT GAC TGC      106
Asn Pro Leu Ala Ala Pro Leu Leu Ile Leu Trp Phe His Leu Asp Cys
      -15                      -10                      -5

GTG AGC AGC ATA CTG AAC GTG GAA CAA AGT CCT CAG TCA CTG CAT GTT      154
Val Ser Ser Ile Leu Asn Val Glu Gln Ser Pro Gln Ser Leu His Val
      1                      5                      10

CAG GAG GGA GAC AGC ACC AAT TTC ACC TGC AGC TTC CCT TCC AGC AAT      202
Gln Glu Gly Asp Ser Thr Asn Phe Thr Cys Ser Phe Pro Ser Ser Asn
      15                      20                      25

TTT TAT GCC TTA CAC TGG TAC AGA TGG GAA ACT GCA AAA AGC CCC GAG      250
Phe Tyr Ala Leu His Trp Tyr Arg Trp Glu Thr Ala Lys Ser Pro Glu
      30                      35                      40                      45

GCC GTG      256
Ala Val

```

## (2) INFORMATION FOR SEQ ID NO: 314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..455
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.7  
region 1..392  
id HSU32907  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..278  
id H09504  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 410..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 274..318  
id H09504

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 160..455  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..296  
id H17686  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 128..329  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 42..243  
id AA247900  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 85..123  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..39  
id AA247900  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 318..355  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 231..268  
id AA247900  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 128..231  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 22..125  
id R57541  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 231..274  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 124..167  
id R57541  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 312..455  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99



region 1..144  
id N87278  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 345..389  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.3  
seq VVTIVILLCFCKA/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```
AGCTGGGGCC ATGTAATT TA AACCTCTGA AAAGTGTGCT GCGGTCCGTG CACAGCATT 60
GTATAACGTG AGGSGTGAAT GCAGCCCAT CTCTGGAGAA CTTCCTCACA CACCGCAGCM 120
AARGAGAAGG MCTGAAAGAC AAACCTGGGT GCAGCCAGAG AGGTCCAGAT AGATGASCTT 180
GTGGCATCCA TTCCCAAST TCAGCCTAGG GACTCCACGT ACCCCAGCTG GGTCTCAT TG 240
TTCCAGAACT GCATTAGTTA AGATTACCCA GACTTNGATT TCAAAGGAAT ACTTTCATTG 300
TTCCGTCTGT AACACGAAGT AATTGGGGCC AGCTGGATGT CAGG ATG CGT GTG GTT 356
                                     Met Arg Val Val
                                     -15

ACC ATT GTA ATC TTG CTC TGC TTT TGC AAA GCG GCT GAG CTG CGC AAA 404
Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala Glu Leu Arg Lys
-10 -5 1 5

GCA AGC CCA GGC AGT GTG AGA AGC CGA GTG AAT CAT GGC CGG GCG GGT 452
Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His Gly Arg Ala Gly
10 15 20

GGA 455
Gly
```

## (2) INFORMATION FOR SEQ ID NO: 315:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..438  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 100  
region 1..394

id HSU20350  
vrt

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 87..438  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 99  
region 3..352  
id HSU28934  
vrt

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 132..401  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq LLFVATLPFWTHY/LI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```

AAACTCTGCA AATAAAATGC TCTTAGAGGG AAGGAAAGGG AAATACTCGT CTCTGGTAAA   60
GTCTGAGCAG GACAGGGTGG CTGACTGGCA GATCCAGAGG TTCCCTTGGC AGTCCACGCC   120
AGGCCTTCAC C ATG GAT CAG TTC CCT GAA TCA GTG ACA GAA AAC TTT GAG   170
      Met Asp Gln Phe Pro Glu Ser Val Thr Glu Asn Phe Glu
      -90                      -85                      -80

TAC GAT GAT TTG GCT GAG GCC TGT TAT ATT GGG GAC ATC GTG GTC TTT   218
Tyr Asp Asp Leu Ala Glu Ala Cys Tyr Ile Gly Asp Ile Val Val Phe
      -75                      -70                      -65

GGG ACT GTG TTC CTG TCC ATA TTC TAC TCC GTC ATC TTT GCC ATT GGC   266
Gly Thr Val Phe Leu Ser Ile Phe Tyr Ser Val Ile Phe Ala Ile Gly
      -60                      -55                      -50

CTG GTG GGA AAT TTG TTG GTA GTG TTT GCC CTC ACC AAC AGC AAG AAG   314
Leu Val Gly Asn Leu Leu Val Val Phe Ala Leu Thr Asn Ser Lys Lys
      -45                      -40                      -35                      -30

CCC AAG AGT GTC ACC GAC ATT TAC CTC CTG AAC CTG GCC TTG TCT GAT   362
Pro Lys Ser Val Thr Asp Ile Tyr Leu Leu Asn Leu Ala Leu Ser Asp
      -25                      -20                      -15

CTG CTG TTT GTA GCC ACT TTG CCC TTC TGG ACT CAC TAT TTG ATA AAT   410
Leu Leu Phe Val Ala Thr Leu Pro Phe Trp Thr His Tyr Leu Ile Asn
      -10                      -5                      1

GAA AAG GGC CTC CAC AAT GCC ATG TGC   437
Glu Lys Gly Leu His Asn Ala Met Cys
      5                      10

```

## (2) INFORMATION FOR SEQ ID NO: 316:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids  
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -23..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.4  
seq VLALLLFVHYSNG/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Val Phe Val His Leu Tyr Leu Gly Asn Val Leu Ala Leu Leu Leu  
-20 -15 -10

Phe Val His Tyr Ser Asn Gly Asp Glu Ser Ser Asp Pro Gly Pro Gln  
-5 1 5

His Arg Ala  
10

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -29..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.3  
seq FLLCIFLICAALA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Gly Met Cys Phe Ala Ala Glu Ser Asp Val Gln Met Phe Ile Ala  
-25 -20 -15

Phe Leu Leu Cys Ile Phe Leu Ile Cys Ala Ala Leu Ala Ala Gln Lys  
-10 -5 1

Ser Gly  
5

## (2) INFORMATION FOR SEQ ID NO: 318:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11  
seq VLFLFLFWGVSLA/GS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Ala Val Arg Glu Leu Cys Phe Ser Arg Gln Arg Gln Val Leu Phe  
-25 -20 -15

Leu Phe Leu Phe Trp Gly Val Ser Leu Ala Gly Ser Gly Phe Gly Arg  
-10 -5 1 5

Tyr Ser Val Thr Gly  
10

## (2) INFORMATION FOR SEQ ID NO: 319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LILLALATGLVGG/ET

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val  
-15 -10 -5

Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser  
1 5 10  
Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly  
15 20 25 30  
Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu  
35 40 45  
Lys Pro Arg Tyr Gly  
50

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (12) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.7
                        seq LILLALATGLVGG/ET
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val  
-15 -10 -5

Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Asa  
1 5 10

Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly  
15 20 25 30

Ala Thr Leu Ile Ala Pro Arg Trp Leu  
35

(2) INFORMATION FOR SEQ ID NO: 321:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (11) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -30..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.6  
seq SLLLAVLVFFFLFA/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

```

Met Arg Ser Cys Leu Trp Arg Cys Arg His Leu Ser Gln Gly Val Gln
-30          -25          -20          -15

Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala Leu Pro
          -10          -5          1

Ser Xaa Xaa Xaa Xaa Xaa Gln Thr Lys Pro Ser Arg His Gln Arg Thr
          5          10          15

Glu Asn Ile Lys Glu Arg Ser Leu Xaa Ser Leu Ala Lys Pro Lys Ser
20          25          30

Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile Tyr Ala Glu Pro Val
35          40          45          50

Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr Gln Pro Lys Ala His Thr
          55          60          65

Thr Gly Asp Arg Arg Lys Gly
          70

```

## (2) INFORMATION FOR SEQ ID NO: 322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.6  
seq XILLALATGLVGG/EI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

```

Met Arg Ile Leu Gln Xaa Ile Leu Leu Ala Leu Ala Thr Gly Leu Val

```

(11) MOLECULE TYPE: PROTEIN

## (v) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -23..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.2  
seq RCLLLALVAESSS/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Ile Ala Cys Ser Ile Arg Glu Leu His Arg Cys Leu Leu Leu Ala  
-20 -15 -10  
Leu Val Ala Glu Ser Ser Ser Gln Thr His Gly  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (v) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.2  
seq SLVLCLLSATVFS/LQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe  
-15 -10 -5  
Ser Leu Gln Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Pro Gly  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO: 326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3  
seq AMWWLLIWGVQLQX/XP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Pro Gly Pro Arg Val Trp Gly Lys Tyr Leu Trp Arg Ser Pro His  
-35 -30 -25 -20  
Ser Lys Gly Cys Pro Gly Ala Met Trp Trp Leu Leu Leu Trp Gly Val  
-15 -10 -5  
Leu Gln Xaa Xaa Pro Asn Pro Gly Leu Arg Pro Leu Gly Xaa Arg Ala  
1 5 10  
Thr Pro Ala Ala Asp Ile Pro Arg Val Pro Arg Ala Val Trp Gln Arg  
15 20 25  
Pro Arg Glu Gln His Gly His Gln Gly Ser Arg Gly Leu Cys Cys Glu  
30 35 40 45  
Ala Arg Leu Pro Gly Leu Arg Pro Gly Ala Val Pro Gly Leu Cys Arg  
50 55 60  
Gly Leu Cys His Asn Leu Ile Arg Arg Phe Gly Ser Lys Pro Leu Gly  
65 70 75

## (2) INFORMATION FOR SEQ ID NO: 327:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq LLTLALLGGPTNX/XX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met His Arg Pro Glu Ala Met Leu Leu Leu Thr Leu Ala Leu Leu  
 -20 -15 -10

Gly Gly Pro Thr Trp Xaa Xaa Lys Met Tyr Gly Pro Gly Gly Gly Lys  
 -5 1 5 10

Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly Leu Arg  
 15 20 25

Val Ser Val Gly Xaa Leu Leu Val Lys Ser Val Gln Val Lys Leu Gly  
 30 35 40

Asp Ser Trp Asp Val Lys Leu Gly Gly Leu Arg Trp Glu Tyr Pro Gly  
 45 50 55

Ser His Pro Ala Ala Arg Arg Ile His His Lys Ser Leu Cys Arg Phe  
 60 65 70

Gln Ala Phe Leu  
 75

## (7) INFORMATION FOR SEQ ID NO: 328:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne method
- (D) OTHER INFORMATION: score 8.6  
 seq SVSLALLSGWVGS/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Met Val Ser Val Ser Leu Ala Leu Leu Ser Gly Trp Val Gly Ser Arg  
 -15 -10 -5 1

Gln Gly Gly Val Gly Leu Ser Thr Leu Val Thr Leu Gly Leu Val Ser  
 5 10 15

Trp Cys Trp Arg Met Val Arg Thr Gln Ala Leu Glu Gly Phe Leu Ser  
 20 25 30

Val Lys Tyr Tyr Ser Ala Phe Ser Ala Asp Leu  
 35 40

## (2) INFORMATION FOR SEQ ID NO: 329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq IVFLLLRVSPCLG/PS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

```

Met His Ile Phe Ser Ile Cys Cys Met Xaa Ser Glu Leu His Lys Met
      -45                      -40                      -35

Lys Ser Leu Ser Leu Gln Leu Ala Ser Glu Lys Arg Ser Leu Val Ala
      -30                      -25                      -20

Leu Val Glu Glu Ile Val Phe Leu Leu Leu Arg Val Ser Pro Cys Leu
      -15                      -10                      -5

Gly Pro Ser Xaa Lys Pro Arg
      1                      5

```

## (2) INFORMATION FOR SEQ ID NO: 330:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq VSALLMAWFGVLS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

```

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu
      -15                      -10                      -5

```

Ser Cys Val Gln Thr Gly  
 1 5

## (2) INFORMATION FOR SEQ ID NO: 331:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq LLLPLMLMSMVSS/SL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Pro Leu Met Leu  
 -20 -15 -10  
 Met Ser Met Val Ser Ser Ser Leu Xaa Pro Gly Val Ala Arg Gly His  
 -5 1 5 10  
 Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Gln Gly Gly Leu  
 15 20 25

## (2) INFORMATION FOR SEQ ID NO: 332:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq LLLPLMLMSXVSS/SL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

```

Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met Leu
  -20                      -15                      -10

Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg Gly His
  -5                      1                      5                      10

Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln
          15                      20                      25

Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe
          30                      35                      40

Met Thr Val Ser Gly
          45

```

## (2) INFORMATION FOR SEQ ID NO: 333:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2  
seq LLLQLSLPSPTS/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

```

Met Leu Leu Leu Leu Gln Leu Ser Leu Pro Ser Pro Thr Ser Ser Pro
          -10                      -5                      1

```

## (2) INFORMATION FOR SEQ ID NO: 334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -17..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.1  
 seq LSFKLLLLAVALG/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Met Leu Lys Met Leu Ser Phe Lys Leu Leu Leu Leu Ala Val Ala Leu  
 -15 -10 -5

Gly Phe Phe Glu Gly Asp Ala Lys Phe Gly Glu  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -22..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8  
 seq LLTLALLGXXXWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu Leu  
 -20 -15 -10

Gly Xaa Xaa Xaa Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys  
 -5 1 5 10

Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly Leu Arg  
 15 20 25

Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln Val Lys Leu Gly  
 30 35 40

Asp Ser Trp Asp Val  
 45

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8  
seq VSAVLGVCAAAWC/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp Cys  
-15 -10 -5  
Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly Gly Arg  
1 5 10 15  
Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Thr Ile  
20 25 30  
Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys Phe Arg Asp Asp  
35 40 45  
Asp Tyr Phe Arg Thr Gly  
50

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.8  
seq VLWLISFFTFDDG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp  
-15 -10 -5

Gly His Gly Gly Phe Leu Gly Lys Asn Asp Gly Ile Lys Thr Lys Lys  
 1 5 10 15  
 Glu Leu Ile Val Asn Lys Lys Lys His Leu Gly Leu Gly  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7  
seq ILDDLICLLFITA/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Cys Ile Ile Leu Leu Asp Leu Ile Cys Leu Leu Phe Ile Thr Ala  
 -15 -10 -5  
 Cys Val Gly  
 1

## (2) INFORMATION FOR SEQ ID NO: 339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -59..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FMVFGSFFFLISC/QP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:



```

Met Asp Cys Ala Ser Ile Ser Val Lys Phe Thr Ser Met Ala Thr Met
      -55                      -50                      -45

His Asp Leu Ser Gln Phe Trp Ala Ser Arg Gly Glu Val Thr Asn Trp
      -40                      -35                      -30

Trp Pro Val Gly Gln Thr Ser Leu Pro Leu Phe Tyr Leu Ala Phe Met
      -25                      -20                      -15

Val Phe Gly Ser Phe Phe Pro Leu Ile Ser Cys Gln Pro Gly
      -10                      -5                      1

```

## (2) INFORMATION FOR SEQ ID NO: 340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq LVVLEFGITAGTG/AK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

```

Met Thr Ala Ser Pro Asp Tyr Leu Val Val Leu Phe Gly Ile Thr Ala
-20      -15      -10      -5

Gly Ala Thr Gly Ala Lys Leu Gly Ser Asp Glu Lys Glu Leu Ile Leu
      1          5          10

Leu Phe Trp Lys Val Val Asp Leu Ala Asn Lys Lys Val Gly Gln Leu
      15      20      25

His Glu Xaa Xaa Leu Asp Arg Ile Trp
      30      35

```

## (2) INFORMATION FOR SEQ ID NO: 341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -15..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.6  
 seq CVLVLAAGAVA/VF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

```

Met Val Cys Val Leu Val Leu Ala Ala Ala Ala Gly Ala Val Ala Val
-15              -10              -5              1
Phe Leu Ile Leu Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr
      5              10              15
Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His
      20              25              30
Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser
      35              40              45
Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met Ser Ala Thr
      50              55              60

```

## (2) INFORMATION FOR SEQ ID NO: 342:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -44..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.5  
 seq LMIPLLLTPITA/TS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

```

Met Lys Lys Thr Gly Asp Gly Gly Thr Leu Ser Thr Glu Arg Ile Gly
      -40              -35              -30
Gly Ala Ala Leu Leu Ser Leu Leu Leu Lys Arg Met Lys Met Thr Leu
      -25              -20              -15

```

```

Met Ile Pro Leu Leu Leu Leu Thr Pro Ile Thr Ala Thr Ser Thr Ser
  -10                -5                1

Arg Trp Pro Glu Ile Gly Val Val Ala Ile Arg Ser Gln Leu Arg Ala
  5                10                15                20

Leu His Thr Cys Gly Gln Glu Pro Val Pro Ala Met Gly Ser Glu Gly
                25                30                35

Ala Ala

```

## (2) INFORMATION FOR SEQ ID NO: 343:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (11) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (1x) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5  
seq LTFLQLLLISSLP/RE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

```

Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Leu
  -20                -15                -10

Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn Glu Ala
  -5                1                5

Cys Pro Gly Ala Glu Trp Xaa Ile Met Cys Arg Glu Cys Cys Glu Tyr
  10                15                20                25

Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu Val Val Gly Tyr
                30                35                40

Thr Ile Pro Cys Cys Arg Asn Glu Xaa Asn Glu Cys Asp Ser Cys Leu
                45                50                55

Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys Xaa Ser Cys Arg Asn
                60                65                70

Gly Ser Trp Gly Gly Thr Leu
  75                80

```

## (2) INFORMATION FOR SEQ ID NO: 344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq SLLFFLLLEGXTEQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

```
Met Arg Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu
   -25                      -20                      -15

Leu Phe Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His
   -10                      -5                      1                      5

Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu
          10                      15                      20

Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn
          25                      30                      35

Cys Ile Cys Ser Glu Xaa Gly Asn Val Leu Cys Ser Arg Val Arg Cys
   40                      45                      50
```

## (2) INFORMATION FOR SEQ ID NO: 345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq VQIMLLLVTVSDC/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val  
                   -15                  -10                  -5

Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys  
                   1                  5                  10

Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg  
           15                  20                  25

Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser  
   30                  35                  40                  45

His Lys Ile Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys  
                   50                  55                  60

Leu

## (2) INFORMATION FOR SEQ ID NO: 346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq SALLFSLLEAST/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu  
   -20                  -15                  -10

Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro  
   -5                  1                  5                  10

Xaa Thr Asn Asn Phe Xaa Asp Xaa Glu Ala Ala Leu Lys Ala His  
           15                  20                  25

## (2) INFORMATION FOR SEQ ID NO: 347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.2  
seq SALLPSLLCEAST/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu  
-20 -15 -10  
Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro  
-5 1 5 10  
Pro Thr Asn Asn Phe Thr Asp Ile Glu Ala Ala Leu Lys Ala Gln Leu  
15 20 25  
Asp Ser Ala Asp Ile Pro Lys Ala Arg Arg Lys Arg Tyr Ile Ser Gln  
30 35 40  
Asn Asp Met Ile Ala Ile Leu Asp Tyr His Asn Gln Val Arg Gly Lys  
45 50 55  
Val Phe Pro Xaa Ala  
60

## (2) INFORMATION FOR SEQ ID NO: 348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.2  
seq LLTLVLCVAVAYE/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Asp Pro Asn Gly Gly Cys Cys Thr Leu Leu Thr Leu Val Leu Cys  
-20 -15 -10

Val Ala Val Ala Tyr Glu Arg Gln Glu  
-5 1

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq LFTFSTSLPSSL3/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Glu Gly Glu Ile Tyr Phe Gln Val Phe Leu Ser Leu Phe Thr Phe  
-25 -20 -15 -10

Ser Thr Ser Leu Pro Ser Ser Leu Ser Ser Ser Ser Leu Ser Ser Ser  
-5 1 5

Asn Gly

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq FLCMLAAIDLAL3/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val  
 -40 -35 -30

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
 -25 -20 -15 -10

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met  
 -5 1

## (2) INFORMATION FOR SEQ ID NO: 351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq PWFLAPWCPGTQS/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Arg Glu Thr Xaa Pro Leu Pro Lys Pro Leu Lys Asp Thr Ala Pro  
 -40 -35 -30

Ser Ser His Gly Val Gly Ser Asp Ser Pro Ser Ala Thr Arg Pro Trp  
 -25 -20 -15

Phe Leu Ala Pro Trp Cys Pro Gly Thr Gln Ser Asn Arg Ile Cys His  
 -10 -5 1 5

Pro Pro Leu Ser Ser Pro Pro Asp Gln Ala Thr Cys Leu Arg Gly  
 10 15 20

## (2) INFORMATION FOR SEQ ID NO: 352:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate



## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq VLVVLALRSLGRS/CS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

```

Met Asp Arg Pro Gly Ser Leu Ser Val Phe Gly Ser Leu Pro Ala Ser
-60                -55                -50                -45

Leu Gly Thr Trp Leu Ser Ser Pro Ala Trp Leu Val Asp Arg Pro Val
                -40                -35                -30

Arg Ser Ala His Pro Ser Ala Asn Ser Thr Gly Val Arg Met Ser Val
                -25                -20                -15

Leu Val Val Leu Ala Leu Arg Ser Leu Gly Arg Ser Cys Ser Leu Ser
                -10                -5                1

Gln Ala Ala Pro Ser Arg Trp Thr Arg Ser Asn Asp Ala Pro Gln Pro
 5                10                15                20

Pro Gly Ser Gln His Ile Phe His Thr Xaa Val Pro Gly
                25                30

```

## (2) INFORMATION FOR SEQ ID NO: 353:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq VILLESYPSCCLC/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

```

Met His Tyr Phe Val Ala Gly Lys Val Ile Leu Leu Phe Ser Tyr Pro
-20                -15                -10

Ser Cys Cys Leu Cys Phe Leu Val Tyr Arg Arg Val Ser Xaa Leu Phe
-5                1                5                10

Lys Cys Phe Glu
                15

```

## (2) INFORMATION FOR SEQ ID NO: 354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq STVVLQVLTQATS/QD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Asp Leu Asn Ser Ala Ser Thr Val Val Leu Gln Val Leu Thr Gln  
                  -15                  -10                  -5

Ala Thr Ser Gln Asp Thr Ala Val Leu Lys Pro Ala Glu Glu Gln Leu  
                  1                  5                  10

Lys Gln Trp Glu Thr Gln Pro Gly Phe Tyr Ser Val Leu Leu Asn Ile  
          15                  20                  25

Phe Thr Asn His Gly  
          30

## (2) INFORMATION FOR SEQ ID NO: 355:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq FLCMLAAIDLALS/TS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
      -70                -65                -60

Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
      -55                -50                -45

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
      -40                -35                -30

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
      -25                -20                -15                -10

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met
      -5                i

```

## (2) INFORMATION FOR SEQ ID NO: 356:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq PLFFSCSISATHS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

```

Met Tyr Arg Leu Ser Leu Ile Ala Gly Pro Gly Ser Tyr Pro Val Leu
      -55                -50                -45

Arg Trp Gly Val Trp Asp Ile Pro Ser Ser Leu Val Gln Val Thr Tyr
      -40                -35                -30                -25

His Gln Pro Asn Leu Thr Thr Asn Leu Asp Leu Pro Leu Phe Phe Ser
      -20                -15                -10

Cys Ser Ile Ser Ala Thr His Ser Cys Val Lys Pro Pro Ser Val Ile
      -5                1                5

Ile Gly Ile Ser Ser Phe Leu Ser Phe Pro Tyr Gln Thr Leu Val
      10                15                20

```

## (1) INFORMATION FOR SEQ ID NO: 357:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(2x) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.9  
seq LCFLSLAVAMSEFF/GS

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu  
-20 -15 -10

Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu  
-5 1 5

Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly  
10 15 20

Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met  
25 30 35 40

Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe  
45 50 55

Pro Pro Ser Met His Phe Phe Gln Ala Lys Trp  
60 65

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids  
(B) TYPE: AMINO ACID  
(C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -35..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.9  
seq XLXXLLTPPSYG/HQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

```

Met Pro Cys Ser Leu Thr Trp Arg Leu Pro Pro Arg Thr Cys Gln Xaa
-35          -30          -25          -20

Xaa Gly Leu Xaa Lys Ser Xaa Leu Xaa Xaa Leu Leu Thr Pro Pro Pro
          -15          -10          -5

Ser Tyr Gly His Gln Pro Gln Thr Gly Ser Gly Glu Ser Xaa Gly Ala
          1          5          10

Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys
          15          20          25

```

## (2) INFORMATION FOR SEQ ID NO: 359:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8  
seq LFLFLTSIAEXCS/TP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Val Xaa Trp Leu Val Leu Phe Ala Leu Gln Ile Tyr Ser Tyr Xaa
-40          -35          -30

Ser Thr Arg Asp Gln Pro Ala Ser Arg Xaa Arg Leu Leu Phe Leu Phe
-25          -20          -15          -10

Leu Thr Ser Ile Ala Glu Xaa Cys Ser Thr Pro Tyr Ser Leu Leu Gly
          -5          1          5

Xaa Val Phe Thr Val Ser Phe Val Ala Leu Gly Val Leu Thr Leu Cys
          10          15          20

Lys Phe Tyr Leu Gln Gly Tyr Arg Ala Phe Met Asn Asp Pro Ala Met
          25          30          35

Asn Arg Gly Gly Ala
          40

```

## (2) INFORMATION FOR SEQ ID NO: 360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq LPDLXXXSLPVGA/WL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

```

Met Ala Arg His Gly Leu Pro Leu Leu Xaa Xaa Xaa Ser Leu Pro Val
      -15                -10                -5

Gly Ala Trp Leu
      1

```

## (2) INFORMATION FOR SEQ ID NO: 361:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq ILYILWYCSVCSS/GS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

```

Met Val His Leu Arg Thr Gly Leu Met Leu Met Ser Ala Asp Arg Leu
      -35                -30                -25

Arg Thr Leu Tyr Tyr Thr Val Thr Ile Leu Tyr Ile Leu Trp Tyr Cys
      -20                -15                -10

Ser Val Cys Ser Ser Gly Ser Leu Leu Ser Thr Ser Ile Met Lys Lys
      -5                1                5                10

```

Arg Met

(2) INFORMATION FOR SEQ ID NO: 362:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (11) MOLECULE TYPE: PROTEIN

(v2) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq ILSTVTALTFFAA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Arg Ala Leu  
-15 -10 -5 1

Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser Glu Lys His Arg  
5 10 15

Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser Ala Pro Gly Ser  
20 25 30

Thr Gln Gln  
35

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (11) MOLECULE TYPE: PROTEIN

(v2) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(IX) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
                        seq LTFLOXLLLISSLK/RE
```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

Met Glu Leu Gly Cys Trp Thr Glu Leu Gly Leu Thr Phe Leu Gln Xaa  
                   -20                  -15                  -10

Leu Leu Ile Ser Ser Leu Xaa Arg Glu Tyr Thr Val Ile Asn Glu Ala  
                   -5                  1                  5

Arg Lys  
           10

## (2) INFORMATION FOR SEQ ID NO: 364:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
                                   seq FLLCXSVFTDCKG/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Glu Leu Leu Arg Val Cys Ser Phe Phe Leu Leu Cys Xaa Ser Val  
                   -20                  -15                  -10

Phe Thr Asp Cys Lys Gly Asp Val Leu Cys Val Lys Met Glu Gln Ser  
                   -5                  1                  5                  10

Gln Ile Cys Ala

## (2) INFORMATION FOR SEQ ID NO: 365:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate



## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq TWFLLLPPGQCRA/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Ile Val Arg Pro Arg Leu Asn Leu Thr Trp Phe Leu Leu Leu Pro  
-20 -15 -10

Pro Gly Gln Cys Arg Ala Val Gly Ala Thr Trp Pro Gly  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 366:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq MVALCCCLWKISG/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu Trp Lys  
-15 -10 -5

Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu Lys Cys  
1 5 10

Leu Leu Asp Lys Ala His Val Gly  
15 20

## (2) INFORMATION FOR SEQ ID NO: 367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq CVCAAXXSQSLX/XX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

```

Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Xaa Xaa
-20                      -15                      -10

Ser Gln Ser Leu Xaa Xaa Xaa Ala Ala Val Ala Ala Ala Gly Gly Arg
-5                      1                      5                      10

Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Xaa Ile
15                      20                      25

Ser Gln Tyr Asp Lys Glu Xaa Gly Xaa Trp Asn Lys Phe Arg Asp Asp
30                      35                      40

Xaa Tyr
45

```

## (2) INFORMATION FOR SEQ ID NO: 368:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq MVALCCCLWKISG/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu
-20                      -15                      -10

Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu
-5                      1                      5                      10

Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys Gly

```

15

20

25

Tyr Ile Phe Ser Leu Ile Ser Pro Gly  
30 35

## (2) INFORMATION FOR SEQ ID NO: 369:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq LWILLGSLSCRTS/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Ala Gln His Leu Trp Ile Leu Leu Gly Ser Leu Ser Cys Arg Thr  
-15 -10 -5

Ser Asn Arg Arg  
1

## (2) INFORMATION FOR SEQ ID NO: 370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq LYLFGSGFWTFXLG/KF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

```

Met Asn Lys Glu Xaa Val Ser Xaa Glu Arg Xaa Ala Gln Val Arg Leu
   -25                      -20                      -15

Tyr Leu Phe Ser Gly Phe Trp Thr Phe Xaa Leu Gly Lys Phe Lys Gln
   -10                      -5                      1

Gly Glu Xaa Ser Tyr Xaa Xaa Ile Leu Glu Arg Leu Leu Trp Gln Gln
   5                      10                      15                      20

Gln Tyr Xaa Gly Trp Leu Val Gly Asp Lys Arg
   25                      30

```

## (2) INFORMATION FOR SEQ ID NO: 371:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq IVFIFLILLNTAA/QV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

```

Met Val Leu Trp Arg Ala Lys Ile Xaa Arg Asn Val Pro Val Thr Leu
   -50                      -45                      -40

Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys
   -35                      -30                      -25

Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile
   -20                      -15                      -10

Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp
   -5                      1                      5                      10

Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn
   15                      20                      25

```

## (2) INFORMATION FOR SEQ ID NO: 372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6  
seq FTSVLWLTSPSQP/NT
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Leu Leu Xaa Phe Phe Thr Ser Val Leu Trp Leu Thr Ser Pro Ser  
-15 -10 -5

Gln Pro Asn Thr Cys Pro Ser Ser Leu Leu Cys Thr Tyr Pro Asn Leu  
1 5 10

Asn Pro Pro Trp  
15

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq IILGCLALFLLLQ/RK
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala  
-20 -15 -10

Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Trp  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq TWLGLLSFQNLHC/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly  
-45 -40 -35  
Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser  
-30 -25 -20  
Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe  
-15 -10 -5 1  
Pro Asp Leu Pro Gly  
5

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq NTLFLRLSGLSAA/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Thr Trp Val Arg His Ala Pro Gly Lys Ser Leu Glu Trp Val Ala  
-55 -50 -45  
Tor Val Thr Asp Gly Gly Asp Lys Thr Phe Tyr Ala Ala Ser Val Lys

-40                      -35                      -30                      -25

Gly Arg Phe Asn Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu  
                          -20                      -15                      -10

His Leu Ser Gly Leu Ser Ala Ala Asp Thr Gly Trp Trp Gly Ile  
                          -5                      1                      5

## (2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (F) TISSUE TYPE: Prostate
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -14..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 5.8  
seq LTSFFSLTANCQS/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

Met Leu Thr Ser Phe Phe Ser Leu Thr Ala Asn Cys Gln Ser Ala Gly  
                          -10                      -5                      1

Thr Ile Ser Phe Ala Ala Phe Ser Leu Met Pro Gly  
                          5                      10

## (2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -18..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 5.8  
seq LTPLFFMXPTGFS/SP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

Met Leu Leu Cys Leu Leu Thr Pro Leu Phe Phe Met Xaa Pro Thr Gly  
-15 -10 -5  
Phe Ser Ser Pro Ser Pro Gly  
1 5

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq HSLFLSLLGLCPS/KT

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Asp Asp Asp Tyr Glu Ala Tyr His Ser Leu Phe Leu Ser Leu Leu  
-20 -15 -10  
Gly Leu Cys Pro Ser Lys Thr Pro Ile Asn Glu Asn Ala Pro Val Phe  
-5 1 5 10  
Asp Pro Glu Pro Val  
15

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1



(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.7  
 seq WLVWLLLGHMVVS/QM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Glu Trp Gly Lys Gln Trp Leu Val Trp Leu Leu Leu Gly His Met  
                   -15                                  -10                                  -5  
 Val Val Ser Gln Met Ala Thr Leu Leu Ala Arg Lys His Arg Pro Trp  
                   1  5  10

(2) INFORMATION FOR SEQ ID NO: 380:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -39..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.7  
 seq LTQGVWLWILVIQA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

Met Arg Arg Gly Lys Arg Leu Leu Glu Ser Gln Ser Ser Ser Pro Lys  
                   -35                                  -30                                  -25  
 Ala Cys Leu Gln Leu Gly Phe Glu Thr Glu Leu Thr Gln Gly Val Leu  
                   -20                                  -15                                  -10  
 Trp Ile Leu Val Ile Gln Ala Val Pro Val Pro Ser Leu Thr Lys Thr  
                   -5  1  5  
 Lys  
   10

(2) INFORMATION FOR SEQ ID NO: 381:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20...-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq ALLESVVWLPCRG/RG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Val Ala Ala Thr Glu Ala Ala Leu Leu Glu Ser Val Val Trp Leu  
-20 -15 -10 -5  
Pro Cys His Gly Arg Gly Gly Ser  
1

## (2) INFORMATION FOR SEQ ID NO: 382:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19...-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq VSLPLLSSWGSTA/WT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Ser Trp Asn Pro Ser Val Ser Leu Pro Leu Leu Ser Ser Trp Gly  
-15 -10 -5  
Ser Thr Ala Trp Thr Leu  
1

## (2) INFORMATION FOR SEQ ID NO: 383:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22...-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq LILLSLHLERRWT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```

Met Lys Arg Ile Gln Gly Ile Leu Phe Leu Ile Leu Leu Ser Leu His
-20                               -15                               -10

Leu Glu Arg Arg Trp Thr Ser Pro Ser Asp His Ser Leu Leu Leu Gly
-5                               1                               5                               10

Gly Asn Ser Leu Ala Gln His Ala Glu Ser Val Val Arg Gln Gly
15                               20                               25

```

## (2) INFORMATION FOR SEQ ID NO: 384:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -35...-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.5  
seq LLTFGLEVCLAAG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

```

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
-35                               -30                               -25                               -20

Gln Leu Xaa Leu Xaa Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
-15                               -10                               -5

Ala Ala Gly Ser Pro Met Cys Arg Leu Cys Cys Trp Lys Trp
1                               5                               10

```

## (2) INFORMATION FOR SEQ ID NO: 385:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq PFALVTSCSSVFS/GD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Ala Ala Gly Val Pro Phe Ala Leu Val Thr Ser Cys Ser Ser Val  
-15 -10 -5

Phe Ser Gly Asp Gln Leu Val Gln His Ile Leu Gly Thr Glu Asp Leu  
1 5 10

Ile Val Glu Val Thr Ser Asn Asp Ala Val Arg Phe Tyr Pro Trp Thr  
15 20 25 30

Ile Asp Asn Lys Tyr Tyr Ser Ala Asp Ile Asn Leu Cys Val Val Pro  
35 40 45

Asn Lys Phe Leu Val Thr Ala Glu Ile Ala Glu Ser Val Gln Ala Phe  
50 55 60

Val Val Tyr Phe Asp Xaa Thr Gln Xaa Ser Gly Leu Asp Ser Val Ser  
65 70 75

Ser Trp Leu Pro Leu Ala Lys Ala Trp Leu Pro Glu Val Met Ile Leu  
80 85 90

Val Cys Asp Arg Val Ser Glu Asp Gly Ile  
95 100

## (2) INFORMATION FOR SEQ ID NO: 386:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -14..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.5  
 seq TVFLXFCFPRCHS/DS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Thr Val Phe Leu Xaa Phe Cys Phe Pro Arg Cys His Ser Asp Ser  
                   -10                  -5                  1  
 His Xaa Xaa Gln Gln Ser Ala  
                   5

## (2) INFORMATION FOR SEQ ID NO: 387:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids  
 (B) TYPE: AMINO ACID  
 (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -48..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.4  
 seq ILLEVFVWNLQG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Met Xaa Pro Asn Asn Phe Trp Gln Lys Leu Gly Arg Lys Lys Pro Arg  
                   -45                  -40                  -35  
 Ile Phe Thr Cys Thr Gln Ser Ser Thr Gly Glu Ala Ala Val Lys Ala  
                   -30                  -25                  -20  
 Glu Asn Leu Ile Leu Leu Glu Val Phe Val Trp Asn Gly Leu Gln Gly  
                   -15                  -10                  -5  
 Leu Pro Ser Glu Leu Ser Asp Thr Ser Gly Ser Ser Lys Lys Leu Gly  
                   1                  5                  10                  15  
 Ser Leu Val Gly Trp Trp Arg Thr Leu Lys Met Ala Pro Ala Cys Leu  
                   20                  25                  30  
 Trp Ser Met Trp Glu Ser Pro Pro Arg  
                   35                  40

## (2) INFORMATION FOR SEQ ID NO: 388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq ALYIMCVPHSVWG/CA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Phe Arg Ser Asp Arg Met Trp Xaa Cys His Trp Lys Trp Lys Pro  
-35 -30 -25

Ser Pro Ieu Leu Phe Leu Phe Ala Leu Tyr Ile Met Cys Val Pro His  
-20 -15 -10 -5

Ser Val Trp Gly Cys Ala Asn Cys Arg Val Val Leu Ser Asn Pro Ser  
1 5 10

Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser Gln  
15 20 25

Ala Cys Met Trp Thr Leu Arg Asp Pro  
30 35

## (2) INFORMATION FOR SEQ ID NO: 389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq LVALSSELPFLGA/G/

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

```

Met Thr Gln Arg Ser Ile Ala Gly Pro Ile Cys Asn Leu Lys Phe Val
-30          -25          -20

Thr Leu Leu Val Ala Leu Ser Ser Glu Leu Pro Phe Leu Gly Ala Gly
-15          -10          -5          1

Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn
          5          10          15

Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met
          20          25          30

Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val
          35          40          45

Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Gln
          50          55          60

```

## (2) INFORMATION FOR SEQ ID NO: 390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq IIPLLLLLSACN/VH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

```

Met Ile Ile Pro Leu Leu Leu Leu Arg Ser Ala Cys Asn Val His
          -10          -5          1

Leu Pro His Gln Thr Ala Ser Pro Ala Ser Leu Ser Pro Gln Gly Leu
          5          10          15

Ala Trp Gly Leu Leu His Gly Gly Cys Ser Val Thr Val Arg
          20          25          30

```

## (2) INFORMATION FOR SEQ ID NO: 391:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3  
seq VLLLSXNLNLIQ/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Xaa Ser Pro Leu Pro Val Leu Leu Leu Ser Xaa Asn Leu Asn Leu  
-15 -10 -5

Ile Ile Gln Ser Ser  
1

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -46..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2  
seq LLTFLVFTXKLSS/LN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Leu Met Cys Lys Met Leu Lys Ser Gln Lys Asn Cys Gln Glu Asn  
-45 -40 -35

Xaa Xaa Ile Lys Ile Ile Leu Phe Leu Lys Pro Met Cys Ser Pro Gln  
-30 -25 -20 -15

Tyr Leu Leu Thr Phe Leu Val Phe Thr Xaa Lys Leu Ser Ser Leu Asn  
-10 -5 1

Lys Xaa Lys Phe His  
5



## (2) INFORMATION FOR SEQ ID NO: 393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq IIVILHCAASIIS/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

Met Lys Lys Lys Ser Ser Pro Asn Gln Tyr Leu His Ser Ser Leu His  
-50 -45 -40

Xaa Ile Arg Leu Phe Ser Phe Leu His Phe Ser Glu Glu Gly Val Leu  
-35 -30 -25

Leu Leu Ala Ile Asp Leu Lys Ile Ile Val Ile Leu His Cys Ala Ala  
-20 -15 -10 -5

Ser Ile Ile Ser Cys Pro Ser  
1

## (2) INFORMATION FOR SEQ ID NO: 394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq ATSVSLEAQSCFA/WP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

```

Met Phe Ser Cys Phe Phe Ser Thr Ser Leu Ala Thr Ser Val Ser Leu
    -20          -15          -10

Glu Ala Gln Ser Cys Phe Ala Trp Pro Leu Ile Val Ser Phe Pro Gln
    -5          1          5

Gly Ser Leu Leu Ser Pro Phe Leu Leu Met Ser Tyr Asn Leu Ser His
    10          15          20          25

Leu Ile Tyr Ser Gly Glu Leu Asn Gly Arg Leu Tyr Ala Glu Asn Ser
    30          35          40

Gln Ile Cys Ile Cys Ser Pro Ala Gly
    45          50

```

## (2) INFORMATION FOR SEQ ID NO: 395:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -50..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq RTALILAVCCGSA/SI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

```

Met His-His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
-50          -45          -40          -35

Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
    -30          -25          -20

Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
    -15          -10          -5

Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
    1          5          10

Ser Gln Asp Leu Ser Gly Gln Thr Ala Pro Gly
    15          20          25

```

## (2) INFORMATION FOR SEQ ID NO: 396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq IYFFACFQALTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Gln Ala Leu Thr Ser  
-15 -10 -5

Ser Ser Pro Pro Gln  
1

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VSGASGFLPPARS/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Xaa Phe Ser Ser Ser  
-35 -25 -20

Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg  
-15 -10 -5 1

Ile Phe Lys Ile Ile Val Ile Gly Asp Xaa Asn Val Gly Lys Thr Cys  
5 10 15

Leu Ser Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg Thr Glu Ala

20                                      25                                      30  
 Thr Ile Gly Val Asp Phe Arg Glu Arg Ala Val Glu Ile Asp Gly Glu  
     35                                      40                                      45  
 Arg Ile Lys Ile Gln Leu Trp Asp Thr Ala  
     50                                      55

## (2) INFORMATION FOR SEQ ID NO: 398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VSGASGFLPPARS/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Ser Phe Ser Ser Ser  
     -30                                      -25                                      -20  
 Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg  
     -15                                      -10                                      -5                                      1  
 Ile Phe Lys Ile Ile Val Ile Gly Asp Ser Asn Val Xaa Lys Thr Cys  
                     5                                      10                                      15  
 Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg  
             20                                      25                                      30

## (2) INFORMATION FOR SEQ ID NO: 399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -27..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
 seq HLSLILLKPLCLP/NN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Leu Val Leu Gly Ser Pro Leu Leu Gly Pro Leu Leu Trp His Leu  
 -25 -20 -15  
 Ser Leu Ile Leu Leu Lys Pro Leu Cys Leu Pro Asn Asn Leu Pro Leu  
 -10 -5 1 5  
 Ala Leu Gly Arg Cys Leu Cys Leu His Ser  
 10 15

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -55..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
 seq VLFMTTAVDLVIT/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met His Leu Leu Asp Leu Glu Ser Met Gly Lys Ser Ser Asp Gly Lys  
 -55 -50 -45 -40  
 Ser Tyr Val Ile Thr Gly Ser Trp Asn Pro Lys Ser Pro His Phe Gln  
 -35 -30 -25  
 Val Val Asn Glu Glu Thr Pro Lys Asp Lys Val Leu Phe Met Thr Thr  
 -20 -15 -10  
 Ala Val Asp Leu Val Ile Thr Glu Val Gln Glu Pro Val Arg Phe Leu  
 -5 1 5  
 Leu Glu Thr Lys Val Arg Val Cys Ser Pro Asn Glu Arg Leu Phe Trp  
 10 15 20 25  
 Pro Ala

## (2) INFORMATION FOR SEQ ID NO: 401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq VLFVFSSIPLTFL/FQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Glu Asn Leu Lys Asp Phe Tyr Val Leu Phe Val Phe Ser Ser Ile  
-20 -15 -10

Pro Leu Thr Phe Leu Phe Gln Lys Leu Pro Phe Val Trp Ile Xaa Glu  
-5 1 5 10

Glu Thr Leu Glu Thr Trp Tyr Leu Lys Ser Trp  
15 20

## (2) INFORMATION FOR SEQ ID NO: 402:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LSIFSLVLPVCRM/HR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Pro Gln Tyr Cys Leu Ser Ile Phe Ser Leu Val Leu Pro Val Cys  
-15 -10 -5

Arg Met His Arg

1

## (2) INFORMATION FOR SEQ ID NO: 403:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LLAFGTSCSVVLY/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe Cys Cys Pro Asn  
-40 -35 -30

Arg Val Arg Gly Val Leu Asn Trp Ser Ser Gly Pro Arg Gly Leu Leu  
-25 -20 -15

Ala Phe Gly Thr Ser Cys Ser Val Val Leu Tyr Asp Pro Leu Gly Cys  
-10 -5 1 5

Cys Tyr Gln Leu Glu Trp Ser His Arg Pro Phe Arg  
10 15

## (2) INFORMATION FOR SEQ ID NO: 404:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LSWLITWFGHXLS/DF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

```

Met Pro Ile Ile Asp Gln Val Asn Pro Glu Leu His Asp Phe Met Gln
      -35              -30              -25

Ser Ala Glu Val Gly Thr Ile Phe Ala Leu Ser Trp Leu Ile Thr Trp
      -20              -15              -10

Phe Gly His Xaa Leu Ser Asp Phe Arg His Val Val Arg Leu Tyr Asp
      -5              1              5              10

Phe Phe Leu Ala Cys His Pro Leu Met Pro Ile Tyr Phe Ala Ala Val
              15              20              25

Ile Val Leu Tyr Arg Glu Gln
      30

```

## (2) INFORMATION FOR SEQ ID NO: 405:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq GLCVLVPCSXSXX/WR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

```

Met Glu Thr Xaa Cys Pro Cys Cys Cys Cys Pro Cys Xaa Gly Xaa Gly
      -45              -40              -35

Ser Leu Xaa Xaa Lys Pro Val Tyr Glu Leu Gln Val Gln Lys Ser Val
      -30              -25              -20

Thr Val Gln Glu Gly Leu Cys Val Leu Val Pro Cys Ser Xaa Ser Xaa
      -15              -10              -5

Xaa Trp Arg Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe
      1              5              10              15

Arg Asp Gly Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn
      20              25              30

Pro Asp Arg Arg Xaa Lys Xaa Xaa Xaa Xaa Xaa Pro Ile Pro Pro Pro
      35              40              45

```



Trp Gly Cys Pro Glu Glu Glu Leu  
50 55

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq IYFFACFXLTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Xaa Xaa Leu Thr Ser  
-15 -10 -5

Ser Ser Pro Pro His Pro Cys Pro Lys Cys Trp Pro Ser Ser Gly Ser  
1 5 10 15

Ile Pro Leu

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq VLKCLSFSXPSLP/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

Met Gly Arg Gly Glu Arg Arg His Tyr Trp Gly Pro Lys Leu Val Leu  
-25 -20 -15

Lys Cys Leu Ser Phe Ser Xaa Pro Ser Leu Pro Gly Phe Leu Trp Ser  
-10 -5 1 5

Leu

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -52..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.7  
seq LLAKALHLLKSSC/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val Met Ser  
-50 -45 -40

Phe Arg Val Ser Glu Leu Gln Val Leu Leu Gly Phe Ala Gly Arg Asn  
-35 -30 -25

Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu  
-20 - -15 -10 -5

Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr  
1 5 10

Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Leu  
15 20 25

Lys

(2) INFORMATION FOR SEQ ID NO: 409:

## (2) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (21) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -69..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq LGPSLSSLPSALS/LM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```

Met His His Arg Met Asn Glu Met Asn Leu Ser Pro Val Gly Met Glu
      -65                      -60                      -55

Gln Leu Thr Ser Ser Ser Val Ser Asn Ala Leu Pro Val Ser Gly Ser
      -50                      -45                      -40

His Leu Gly Leu Ala Ala Ser Pro Thr His Ser Ala Ile Pro Ala Pro
      -35                      -30                      -25

Gly Leu Pro Val Ala Ile Pro Asn Leu Gly Pro Ser Leu Ser Ser Leu
      -20                      -15                      -10

Pro Ser Ala Leu Ser Leu Met Leu Pro Met Gly Xaa Gly Asp Arg Gly
      -5                      1                      5                      10

Val Met Cys Gly Leu
      15

```

## (2) INFORMATION FOR SEQ ID NO: 410:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq IWNLFSLFSTST/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

```

Met Leu His Ser Asp Asn Ile Trp Asn Leu Phe Ser Leu Phe Ser Thr
      -15                      -10                      -5

```

Ser Thr Thr Leu Pro Arg  
1

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq FHSAAGWSGGGQA/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Gln Pro Ala Ser Pro Pro Ala Arg Trp Ser Phe His Ser Ala Ala  
-20 -15 -10  
Gly Trp Ser Gly Gly Gly Gln Ala Cys Gly Gly His Ser Cys Asp Gln  
-5 1 5  
Val Leu Ala Val Ile Glu Leu Leu Asn Pro Leu Arg  
10 15 20

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq LLAGSISHMFSQA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Cys Phe Ser Phe Leu Leu Ala Gly Ser Ile Ser His Met Phe Ser  
-15 -10 -5

Gln Ala Leu Pro Leu His Ser Pro Gly Leu Pro Thr Thr Asn Arg Thr  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq SILFHCSVCLFLC/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Tyr Gly Phe Ile Ile Gly Leu Ser Ile Leu Phe His Cys Ser Val  
-20 -15 -10

Cys Leu Phe Leu Cys Gln Tyr His Ala Trp  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq SLLGCKLAININT/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Ser Phe Gly Xaa Ile Leu Thr Phe Arg Val Ser Leu Leu Gly Cys  
                -20                    -15                    -10

Xaa Leu Ala Ile Asn Ile Asn Thr Phe Pro Ser Asn Asn His Leu  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 415:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(L) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Prostate

## (18) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -22..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4  
seq LGRLCAGSSGVXG/AR

seq LGRLCAGSSGVXG/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala Gly  
-20 -15 -10

Ser Ser Gly Val Xaa Gly Ala Arg Ala Xaa Leu Ser Arg Ser Trp Gln  
-5 1 5 10

Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg Glu Val Asp  
15 20 25

Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr Val Gln Gly Cys  
30 35 40

Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly Gln Cys Leu Glu Thr  
45 50 55

Thr Ala Gln Arg Val Pro  
60

## (2) INFORMATION FOR SEQ ID NO: 416:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (22) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -23..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq LVSIFFFWVTNA/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Phe Asn Thr Ile Tyr Leu Val Ile Ser Leu Val Ser Ile Phe Phe  
-20 -15 -10  
Phe Trp Glu Val Thr Asn Ala Phe Leu Lys Ala Arg Arg Trp  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 417:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq SLPLTTGSSWSLS/SQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Leu Pro Pro Lys Gly Cys Gly Ser Leu Pro Leu Thr Thr Gly  
-20 -15 -10  
Ser Ser Trp Ser Leu Ser Ser Gln Ile Gly Ser Pro Ala Ile Ser Asn  
-5 1 5 10  
Pro Arg

## (2) INFORMATION FOR SEQ ID NO: 418:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids  
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -16..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3  
seq ELSWASFLAPLLR/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met Phe Val Phe Leu Ser Trp Ala Ser Phe Leu Ala Pro Leu Leu Arg  
-15 -10 -5

Ser Pro Phe Leu His Cys Leu Met Gly Met Pro Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3  
seq LLSCSP LXPLGKS/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Xaa Met Lys Ser Ala Asn Lys Ile Thr Leu Leu Xaa His His Leu  
-25 -20 -15

Leu Ser Cys Ser Pro Leu Xaa Pro Leu Gly Lys Ser Gly Phe Ser Ser  
-10 -5 1

Cys Gln Arg Leu Gly Lys Arg Ala Leu Val Phe Pro Ile Xaa Lys Xaa  
5 10 15 20

Ile Ile Thr



## (2) INFORMATION FOR SEQ ID NO: 420:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq SFLLLFIVIPQTP/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Cys Asn Tyr Asn Ile Tyr Val Leu Tyr Asn Ile Gly Tyr Leu Tyr  
-30 -25 -20

His Pro Lys Ser Phe Leu Leu Leu Phe Ile Val Ile Pro Gln Thr Pro  
-15 -10 -5

Arg Pro  
1

## (2) INFORMATION FOR SEQ ID NO: 421:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq PLLAAPLLRSLLP/RX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Ala Val Ala Met Val Lys Leu Cys Glu Arg Ala Gly Leu Pro Leu  
-25 -20 -15

Leu Ala Ala Pro Leu Leu Arg Ser Leu Leu Pro Arg Xaa Pro Gln Pro  
 -10 -5 1 5  
 Gly Pro Ala Gln Pro Arg Ser Val Gln Gly Gln Arg Cys Pro Ala Arg  
 10 15 20  
 His Pro Pro Gly Asn Leu Val Cys Glu Arg Gly Ala Xaa Val Asn Gly  
 25 30 35  
 Val Thr Ala Gly Ala Xaa Gly Xaa Leu Arg Gly Leu His Arg Gly Xaa  
 40 45 50  
 Arg Ala Leu Gly Cys Ser Ala His Arg Pro Xaa His Ser Ala Arg Val  
 55 60 65  
 Arg Pro Pro Ala  
 70

## (2) INFORMATION FOR SEQ ID NO: 422:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -122..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq DVLGGLKDVLLA/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Leu Asn Val Val Arg Ala Leu Arg Xaa Pro Gln Trp Cys Ala Glu  
 -120 -115 -110  
 Tyr Cys Leu Ser Ile His Tyr Gln His Gly Gly Val Ile Cys Thr Gln  
 -105 -100 -95  
 Val His Lys Gln Thr Val Val Gln Leu Ala Leu Arg Val Ala Asp Glu  
 -90 -85 -80 -75  
 Met Asp Val Asn Ile Gly His Glu Val Gly Tyr Val Ile Pro Phe Glu  
 -70 -65 -60  
 Asn Cys Cys Thr Asn Glu Thr Ile Leu Arg Tyr Cys Thr Asp Asp Met  
 -55 -50 -45  
 Leu Gln Arg Glu Met Met Ser Asn Pro Phe Leu Gly Ser Tyr Gly Val  
 -40 -35 -30

Ile Ile Leu Asp Asp Ile His Glu Arg Ser Ile Ala Thr Asp Val Leu  
-25 -20 -15  
Leu Gly Leu Leu Lys Asp Val Leu Leu Ala Arg Pro Glu Leu Lys  
-10 -5 1 5

## (2) INFORMATION FOR SEQ ID NO: 423:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq AGLCIGSTSYVHG/DI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met His Ala Gly Leu Glu Arg Xaa Ser Xaa Gln Lys Ala Leu Ala Gly  
-25 -20 -15  
Leu Cys Ile Gly Ser Thr Ser Tyr Val His Gly Asp Ile Leu Arg Thr  
-10 -5 1 5  
Glu Arg

## (2) INFORMATION FOR SEQ ID NO: 424:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq LLGSLSLWRWSAM/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

```

Met Leu Asn Gly Pro Phe Gln His Arg Asn Ser Arg Ile Met Thr His
-35          *   -30          -25          -20

Arg Ser Ala Glu Lys Thr Leu Leu Gly Ser Leu Ser Leu Trp Arg Trp
          -15          -10          -5

Ser Ala Met Glu Pro Thr Asp Arg Cys Thr Arg Val Gly
      1          5          10

```

(2) INFORMATION FOR SEQ ID NO: 425:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

```

Met Arg Val Lys Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg
          -40          -35          -30

Ser Lys Arg Pro Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile
          -25          -20          -15

Ala Val Gly Leu Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn
          -10          -5          1

His Val Lys Arg Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu
      5          10          15          20

Cys Leu Lys Glu Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser
          25          30          35

Asp Ile Trp Leu Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn
          40          45          50

Ser Glu Ser Gln His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu
          55          60          65

Pro His Cys Ile Ile Ile Asn Leu Ser Thr
      70          75

```

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids  
(B) TYPE: AMINO ACID  
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(1X) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
                        seq FSLLLALSMLKGTG/KV
```

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Pro Gln Lys Gly Leu Gly Leu Leu Gly Ile Leu Ser Gly Asp Phe  
-25 -20 -15

Ser Leu Leu Ala Leu Ser Met Leu Lys Gly Thr Gly Lys Val Gly Gly  
-10 -5 1

## (2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -55..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq AALCGISLSQLFP/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln Pro Leu  
-55 -50 -45 -40

Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg  
-35 -30 -25

Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile  
           -20                                  -15                                  -10  
 Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr  
           -5                                  1                                  5  
 Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu Ala Val  
   10                                  15                                  20                                  25  
 Leu Pro Thr Met Thr Ala  
                                   30

## (2) INFORMATION FOR SEQ ID NO: 428:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq LLLSPWVTVPWWS/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Leu Cys Phe Gly Asp Leu Leu Leu Ser Pro Trp Val Thr Val Pro  
                                   -15                                  -10                                  -5  
 Val Trp Ser Ser Ser Pro Trp  
                                   1

## (2) INFORMATION FOR SEQ ID NO: 429:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: -27..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq LIYFLGLAADTYF/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met Gln Glu Asn Ala His Asn Leu Arg Leu Phe Lys Cys Leu Leu Ile  
-25 -20 -15  
Tyr Phe Leu Gly Leu Ala Ala Asp Thr Tyr Phe Arg Ser Lys Arg Lys  
-10 -5 1 5  
Pro Val Ser Phe Val Val Thr Val Xaa Xaa Gly Xaa Tyr Ala Thr Gly  
10 15 20

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -59..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq SVATALFPPLCIS/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met His Thr Cys Ser Leu Pro Cys Leu Leu Phe Ala Gln Leu Leu Glu  
-55 -50 -45  
Phe Cys Ser Phe Pro Pro Asp Val Pro His Asn Cys Ala Pro Ile Val  
-40 -35 -30  
Ser Val Arg Pro Pro Asn Ile Val Ala Ala Phe Glu Gly Cys Ser Val  
-25 -20 -15  
Ala Thr Ala Leu Phe Pro Pro Leu Cys Ile Ser Thr Gly Asn Glu  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids  
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4  
seq PLLGVLEFFQGVYI/VF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

```
Met Gln Gln Arg Gly Ala Ala Gly Ser Arg Gly Cys Ala Leu Phe Pro
    -25                -20                -15

Leu Leu Gly Val Leu Phe Phe Gln Gly Val Tyr Ile Val Phe Ser Leu
    -10                -5                  1

Glu Ile Arg Ala Asp Ala His Val Arg Gly Tyr Val Gly Glu Lys Ile
    5                  10                15                20

Lys Leu Lys Cys Thr Phe Lys Ser Thr Ser Asp Val Thr Asp Lys Leu
                25                30                35

Thr Ile Asp Trp Thr Tyr Arg Pro Pro Ser Ser Ser His Thr Val Ser
    40                45                50

Ile Xaa His Tyr Gln Ser Phe Gln Tyr Pro Thr Thr Ala Gly Thr Phe
    55                60                65
```

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -39..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9  
seq LILNRSLEPTASSS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:



```

Met Xaa Xaa Ser Ile Phe Ile Ser Glu Lys Tyr Gly Leu Cys Pro Ser
      -35              -30              -25

Lys Thr Pro Ile Met Lys Met Leu Pro Ser Leu Ile Leu Asn Arg Ser
      -20              -15              -10

Leu Pro Thr Ala Ser Ser Ser Ser Ser Arg Lys Asp Phe Arg Leu Pro
      -5              1              5

Gln Thr Arg Arg Arg Ile Ile Met Val Pro Arg Lys Glu Asp Gln Thr
      10              15              20              25

Pro Leu Asn Pro Ala Ser Gln Pro Gln Ala Pro Pro Lys Pro Ile Pro
      30              35              40

Ser Xaa Lys Ser Leu Glu Ala Xaa Asp Xaa Xaa Xaa Ser Gln Arg Thr
      45              50              55

Xaa Arg Pro Gly Leu Ser Arg Gly Arg Ser Cys
      60              65

```

## (2) INFORMATION FOR SEQ ID NO: 433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq FFVVVLFSGCKV/IT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

```

Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala
-20              -15              -10              -5

Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Tyr Ile Glu Lys Glu
      1              5              10

Ala Asn Lys Thr Tyr Asn Cys Glu Asn Leu Gly Leu Ser Glu Ile Pro
      15              20              25

Asp Thr Leu Pro Asn Thr Thr Glu Phe Leu Glu Phe Ser Phe Asn Phe
      30              35              40

Leu Pro Thr Ile His Asn Arg Thr Ser Ser Arg
      45              50              55

```

## (2) INFORMATION FOR SEQ ID NO: 434:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -96..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq IMNLTVMMLDTAXG/KX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

```

Met Glu Val Ala Ala Asn Cys Ser Leu Arg Val Lys Arg Pro Leu Leu
  -95                      -90                      -85

Asp Pro Arg Phe Glu Gly Tyr Lys Xaa Ser Leu Glu Pro Leu Pro Cys
-80                      -75                      -70                      -65

Tyr Gln Leu Glu Leu Asp Ala Ala Val Ala Xaa Val Lys Leu Arg Asp
          -60                      -55                      -50

Asp Gln Tyr Thr Leu Glu His Met His Ala Phe Gly Met Tyr Asn Tyr
          -45                      -40                      -35

Leu His Cys Asp Ser Trp Tyr Gln Asp Ser Val Tyr Tyr Ile Asp Thr
          -30                      -25                      -20

Leu Gly Arg Ile Met Asn Leu Thr Val Met Leu Asp Thr Ala Xaa Gly
          -15                      -10                      -5

Lys Xaa Arg Glu Val Phe Arg Leu Leu
  1                      5

```

## (2) INFORMATION FOR SEQ ID NO: 435:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -39..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq VLAIGLLHIVLLS/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

```

Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg Val
      -35                      -30                      -25

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
      -20                      -15                      -10

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
      -5                      1                      5

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
      10                      15                      20                      25

His Thr Val Lys Gly Xaa Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
      30                      35                      40

Arg Leu Leu Xaa His Xaa Xaa Ala Asp Gly Leu Trp Gly Pro Val
      45                      50                      55

```

## (2) INFORMATION FOR SEQ ID NO: 436:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -23..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq SWWTLLSSSPSFM/IS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

```

Met Glu Asn Phe Asn Met Tyr Lys Asn Lys Ser Trp Trp Thr Leu Leu
      -20                      -15                      -10

Ser Ser Ser Pro Ser Phe Met Ile Ser Phe Val Ser Ser Val Leu Pro
      -5                      1                      5

Val Leu Leu Thr Ile Ser Arg Phe Ile Leu Lys Gln Ile Pro Asp Gln
      10                      15                      20                      25

```

## (2) INFORMATION FOR SEQ ID NO: 437:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq VLAIGLLHIVLLS/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

Met Asn Val Gly Thr Xaa His Ser Glu Val Asn Pro Asn Thr Arg Val  
-35 -30 -25

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu  
-20 -15 -10

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val  
-5 1 5

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu  
10 15 20 25

Tyr Thr Val Lys Gly Thr  
30

## (2) INFORMATION FOR SEQ ID NO: 438:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8

seq AAASAVSVLLVAA/ER

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Met Ala Ala Ala Ser Ala Val Ser Val Leu Leu Val Ala Ala Glu Arg  
                   -10                  -5                  1

Asn Arg Trp His Arg Leu Pro Ser Leu Leu Leu Pro Pro Arg Thr Trp  
           5                  10                  15

Val Trp Arg Gln Arg Thr Met Lys Tyr Thr Thr Ala Thr Gly Arg Asn  
       20                  25                  30

Met  
   35

## (2) INFORMATION FOR SEQ ID NO: 439:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
                                   seq SGSGLSWARLSQS/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Ala Tyr Ser Lys Ala Ser Gly Ser Pro Val Leu Ser Gln Ala Val  
                   -40                  -35                  -30

Pro Gly Glu Asn Ala Ser His Arg Arg Gly Ser Ala Asp Leu Gly Ser  
           -25                  -20                  -15

Gly Ser Gly Leu Ser Trp Ala Arg Leu Ser Gln Ser Arg Ser Glu Ile  
       -10                  -5                  1

His Ser Ala Gly Pro Pro His Leu Gly Gly Arg Thr Asn Gly Pro Glu  
       5                  10                  15                  20

Phe Pro Ala Leu Ser Tyr Ser Ser Gln Leu Leu Ser Leu Ala Gln Leu  
           25                  30                  35

Arg Gly Arg Gly Ile Thr Glu Val Ser Glu Lys Ser Pro Leu Ile  
       40                  45                  50

## (2) INFORMATION FOR SEQ ID NO: 440:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq RPVLLHLHQTAHA/DE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

```

Met Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp
  -35                      -30                      -25

Thr Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His
  -20                      -15                      -10

Gln Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His
   -5                      1                      5                      10

Thr Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala
    15                      20                      25

Ile Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile
    30                      35                      40

His Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Gln
   45                      50                      55

```

## (2) INFORMATION FOR SEQ ID NO: 441:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7  
seq IPCAHMLVCPTIG/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```
Met Ile Ile Cys Tyr Asp Ile Pro Cys Ala His Met Leu Val Cys Pro
      -15                -10                -5
Thr Ile Gly Asp Ile Lys Phe Asp His Leu Met Lys Trp Tyr Pro Ser
      1                5                10
Asp Phe Ser Thr Glu Arg Leu
      15                20
```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids  
(B) TYPE: AMINO ACID  
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq STLASVPPAATFG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```
Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala Ala
      -15                -10                -5
Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln Met
      1                5                10
Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro Gln
      15                20                25
Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val Glu
      30                35                40                45
Lys Asn Lys Tyr Asp Ala
      50
```

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -65..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq QLEGLNWLRFSA/QG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Gly Glu Asp Pro Xaa Gln Pro Arg Lys Tyr Lys Lys Xaa Lys Xaa  
-65 -60 -55 -50  
Glu Leu Gln Gly Asp Xaa Pro Pro Ser Ser Pro Thr Asn Asp Pro Thr  
-45 -40 -35  
Val Lys Tyr Glu Thr Gln Pro Arg Phe Ile Thr Ala Thr Gly Gly Thr  
-30 -25 -20  
Leu His Met Tyr Gln Leu Glu Gly Leu Asn Trp Leu Arg Phe Ser Trp  
-15 -10 -5  
Ala Gln Gly Thr Xaa Gly  
1 5

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -42..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq LLGCLQCCWLQSG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Phe Tyr Val Ala Met Thr Lys Thr His Lys Arg Ile Arg Ser Leu  
-40 -35 -30



Cys Asn Ile His His Gly Leu Phe Gln Phe Thr Gln Gln Leu Leu Gly  
   -25                   -20                   -15  
 Cys Leu Gln Cys Cys Trp Leu Gln Ser Gly Arg Ala Pro Ala Thr Tyr  
   -10                   -5                   1                   5  
 Tyr Leu Val Glu Ser Ile Glu Lys Ser Ala His Gly Ser Val Leu Xaa  
           10                   15                   20  
 Thr Tyr Asp Gln Thr Gln Thr Arg Ile Gly Arg  
           25                   30

## (2) INFORMATION FOR SEQ ID NO: 445:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq XTCASXNPSQCLA/AF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Val Ser Pro Lys Asp Leu Pro Leu Val Leu Leu Gln Asp Ile Lys  
   -60                   -55                   -50                   -45  
 Val Pro Ser Ser Met Thr Gly Ser His Ala Gly Asn Pro His Ile Glu  
           -40                   -35                   -30  
 Arg Asn Asp Leu Pro Arg His Gly Ser Pro Gln Phe Phe Thr Gly Xaa  
           -25                   -20                   -15  
 Thr Cys Ala Ser Xaa Asn Pro Ser Gln Cys Leu Ala Ala Phe  
           -10                   -5                   1

## (2) INFORMATION FOR SEQ ID NO: 446:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq FXSLFCLYFSCFL/HI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

Met Glu Phe Xaa Ser Leu Phe Cys Leu Tyr Phe Ser Cys Phe Leu His  
-15 -10 -5 1

Ile Ile Tyr Phe Xaa Ser Cys Phe Leu Tyr  
5 10

## (2) INFORMATION FOR SEQ ID NO: 447:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -45..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq ALLELIDSPECLS/KC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Ala Leu His Phe Gln Ser Leu Ala Glu Leu Glu Xaa Leu Cys Thr  
-45 -40 -35 -30

His Leu Tyr Ile Gly Thr Asp Leu Thr Gln Arg Ile Glu Ala Glu Lys  
-25 -20 -15

Ala Leu Leu Glu Leu Ile Asp Ser Pro Glu Cys Leu Ser Lys Cys Gln  
-10 -5 1

Leu Leu Leu Glu Gln Gly Thr Thr Ser Tyr Ala Gln Leu Leu Ala Ala  
5 10 15

Thr Xaa  
20

## (2) INFORMATION FOR SEQ ID NO: 448:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq LLLLLITPSPSP/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr  
-25 -20 -15  
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly  
-10 -5 1 5  
Leu Ser Leu Arg Ser Ala Met Ser  
10

## (2) INFORMATION FOR SEQ ID NO: 449:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq AVSSLIAGVGTSHG/LA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

Met Arg His Ser Leu Leu Lys Gly Ile Ser Ala Gln Ile Val Ser Ala  
-40 -35 -30

Ala Asp Lys Val Asp Ala Gly Leu Pro Thr Ala Ile Ala Val Ser Ser  
-25 -20 -15 -10  
Leu Ile Ala Val Gly Thr Ser His Gly Leu Ala Gly  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 450:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LSCFIFFYISSLC/CF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Thr Leu Ser Cys Phe Ile Phe Phe Tyr Ile Ser Ser Leu Cys Cys  
-15 -10 -5 1  
Phe Leu Ser Tyr Pro Thr Arg  
5

## (2) INFORMATION FOR SEQ ID NO: 451:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LCFLLPHHRLQEA/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg  
-15 -10 -5 1  
Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg  
5 10 15  
Arg Arg Glu Lys Thr Asn Lys Trp Glu Lys Arg Lys Gly Ser Gly  
20 25 30

## (2) INFORMATION FOR SEQ ID NO: 452:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq FSLFALNMPLGFC/VY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Phe Ser Leu Phe Ala Leu Asn Met Pro Leu Gly Phe Cys Val Tyr  
-10 -5 1  
Val Ile Phe Lys Ile His Asp Trp  
5 10

## (2) INFORMATION FOR SEQ ID NO: 453:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5

seq SVWGVLPSPACSA/DL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

```

Met Ala Ser Ser Pro Gly Val Ala Met His Ser Leu Trp Ala Thr Ile
-30                -25                -20

His Thr Ser Val Trp Gly Val Leu Pro Pro Pro Ala Cys Ser Ala Asp
-15                -10                -5                1

Leu Leu Phe Ser Asn Ala Cys Leu Leu Pro His Glu Ile His Leu
      5                10                15

```

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LPRLLSLSQHSSES/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

```

Met Ser Gln Glu Gly Ala Val Pro Ala Ser Ala Val Pro Leu Glu Glu
-45                -40                -35                -30

Leu Ser Ser Trp Pro Glu Glu Leu Cys Arg Arg Glu Leu Pro Ser Val
      -25                -20                -15

Leu Pro Arg Leu Leu Ser Leu Ser Gln His Ser Glu Ser Trp Ile Glu
      -10                -5                1

His Ile Gln Ile Leu Lys Ile Ile Val Glu Met Phe Leu Pro His Met
      5                10                15

Asn His Leu Thr Leu Glu Gln Thr Phe Phe Ser Gln Val Leu Pro Lys
      20                25                30                35

Thr Val Lys Leu Phe Asp
      40

```

(2) INFORMATION FOR SEQ ID NO: 455:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -36..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
 seq AAVVFAVVLSIHA/TV
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

```

Met Thr Arg Glu Cys Pro Ser Pro Ala Pro Gly Pro Gly Ala Pro Leu
  -35                      -30                      -25

Ser Gly Ser Val Leu Ala Glu Ala Ala Val Val Phe Ala Val Val Leu
  -20                      -15                      -10                      -5

Ser Ile His Ala Thr Val Trp
                      1

```

(2) INFORMATION FOR SEQ ID NO: 456:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 85 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -18..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 14.8  
 seq LLWWALLLGLAQA/CP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

```

Met Gln Glu Leu His Leu Leu Trp Trp Ala Leu Leu Leu Gly Leu Ala
  -15                      -10                      -5

Gln Ala Cys Pro Glu Pro Cys Asp Cys Gly Glu Lys Tyr Gly Phe Gln
  1                      5                      10

```

Ile Ala Asp Cys Ala Tyr Arg Asp Leu Glu Ser Val Pro Pro Gly Phe  
 15 20 25 30  
 Pro Ala Asn Val Thr Thr Leu Ser Leu Ser Ala Asn Arg Leu Pro Gly  
 35 40 45  
 Leu Pro Glu Gly Ala Phe Arg Glu Val Pro Leu Leu Gln Ser Leu Trp  
 50 55 60  
 Leu Ala His Asn Glu  
 65

## (2) INFORMATION FOR SEQ ID NO: 457:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.6  
seq LLLALCATGAQG/LY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Gly Arg Gln Ala Leu Leu Leu Leu Ala Leu Cys Ala Thr Gly Ala  
 -15 -10 -5  
 Gln Gly Leu Tyr Phe His Ile Gly Glu Thr Glu Lys Arg Cys Phe Ile  
 1 5 10  
 Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly Asn Tyr Arg Thr Gln  
 15 20 25 30  
 Met Trp Asp Lys Gln Lys Glu Val Phe Leu Pro Ser Thr Pro Gly Leu  
 35 40 45  
 Gly Met His Val Glu Val Lys Asp Pro Asp Gly Lys Val Val Leu Ser  
 50 55 60  
 Arg Gln Tyr Gly Ser Glu Gly Arg Phe Thr Phe Thr Ser His Xaa Xaa  
 65 70 75  
 Gly Asp His Gln Ile Cys Leu His Cys Gly  
 80 85

## (2) INFORMATION FOR SEQ ID NO: 458:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 40 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -21..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 12.7  
                            seq ILFLLSWGPLQG/QQ
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser  
-20                    -15                    -10

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg  
-5                    1                    5                    10

Arg Leu Ala Ala Leu Glu Glu Arg  
15

(2) INFORMATION FOR SEQ ID NO: 459:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 78 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Prostate
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -27..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 8.8  
                            seq LLLLCPLSRGCCP/LL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Ser Cys Arg Glu Leu Thr His Arg Pro Cys Ser Pro His Leu Leu  
-25                    -20                    -15

Leu Leu Cys Pro Leu Ser Arg Gly Cys Cys Pro Leu Leu Leu Ser Xaa  
-10                    -5                    1                    5

Pro Leu Xaa Gly Val Asn Leu Glu Ser Ile Leu Ser Leu Thr Leu Pro  
                   10                  15                  20

Pro Ser Pro Ser Ser Val Gly Leu Ser Pro Ser Val Thr Xaa Leu Thr  
                   25                  30                  35

Thr Ser Pro Val Ser Leu His Phe Ala Ser Xaa Leu Ala Gly  
           40                  45                  50

## (2) INFORMATION FOR SEQ ID NO: 460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq AALLLGLMMVVTG/DE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu  
       -20                  -15                  -10

Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His  
       -5                  1                  5                  10

Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val  
           15                  20                  25

Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys  
           30                  35                  40

Xaa Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys  
           45                  50                  55

Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp  
           60                  65                  70

Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His  
           75                  80                  85                  90

Trp Leu Val Thr Asp Ile Lys Gly Ala  
           95

## (2) INFORMATION FOR SEQ ID NO: 461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq VHLLSLCSGKVYA/RM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

```

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
      -20                      -15                      -10
Leu Cys Ser Gly Lys Val Tyr Ala Arg Met Ala Ser Leu Arg Gly Leu
      -5                      1                      5
Gly

```

## (2) INFORMATION FOR SEQ ID NO: 462:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq LIFLCGAALLAVG/IW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

```

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
      -25                      -20                      -15
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
      -10                      -5                      1

```

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
           5                          10                          15

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
       20                          25                          30                          35

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
                           40                          45                          50

Glu Ser Lys Cys Ala Leu Val Thr Phe  
                           55                          60

## (2) INFORMATION FOR SEQ ID NO: 463:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq IVSLLGFVATVTL/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile  
           -25                          -20                          -15

Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe  
           -10                          -5                          1

Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys  
       5                          10                          15                          20

Thr Ser Gln

## (2) INFORMATION FOR SEQ ID NO: 464:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq VLMRLVASAYSIA/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

```

Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
      -15                      -10                      -5

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
      1                      5                      10

Gly Asp Leu Gly Ile Val Glu Xaa Thr Cys Ala Thr Asp Leu Gln Thr
      15                      20                      25

Lys Ala Asp Arg Leu Ala Gln Met Xaa Ile Cys Ser Ser Leu Ala Arg
      30                      35                      40                      45

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Xaa
      50                      55                      60

Glu Val Asp Gln Glu
      65

```

## (2) INFORMATION FOR SEQ ID NO: 465:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq VHLLSLCSGKAIC/KN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

```

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
      -20                      -15                      -10

Leu Cys Ser Gly Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr
      -5                      1                      5

```

Phe Glu Glu Ile Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys  
 10 15 20  
 Ala Ile Ile Asn Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr  
 25 30 35 40  
 Xaa Arg Leu Ala Leu Leu Val  
 45

## (2) INFORMATION FOR SEQ ID NO: 466:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq ALXVLP LLGLHEA/AS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met Ala Asp Thr Thr Pro Asn Gly Pro Gln Gly Ala Gly Ala Val Gln  
 -50 -45 -40  
 Phe Met Met Thr Asn Lys Leu Asp Thr Ala Met Trp Leu Ser Arg Leu  
 -35 -30 -25 -20  
 Phe Thr Val Tyr Cys Ser Ala Leu Xaa Val Leu Pro Leu Leu Gly Leu  
 -15 -10 -5  
 His Glu Ala Ala Ser Phe Tyr Gln Arg Ala Leu Leu Ala Asn Ala Leu  
 1 5 10  
 Thr Ser Ala Leu Arg Leu His Gln Arg Leu Pro His Phe Gln Leu Ser  
 15 20 25  
 Arg Ala Phe Leu Ala Gln Ala Leu Leu Glu Asp Ser Cys His Tyr Leu  
 30 35 40 45  
 Leu Tyr Ser Leu Ile Phe Val Asn Ser Tyr Pro Val Thr Met Ser Ile  
 50 55 60  
 Phe Pro Val Leu Leu Phe  
 65

## (2) INFORMATION FOR SEQ ID NO: 467:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq XVLVLSVVXXAMA/AF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Met Arg Phe Arg His Phe Xaa Lys Xaa Ile Gly Xaa Val Leu Val Leu  
                  -20                                  -15                                  -10

Ser Val Val Xaa Xaa Ala Met Ala Ala Phe Ala Val Xaa Pro Gln Gly  
                  -5                                          1                                          5

Pro Ala Leu Xaa Ser Glu Pro Xaa Xaa Xaa Gly Ser Pro Thr Ser Pro  
          10                                  15                                          20

Lys Pro Gly Val Asn Ala Gln Phe Leu Pro Gly Phe Leu Met Gly Xaa  
          25                                  30                                          35                                          40

Leu Pro Ala Pro Val Thr Pro Gln Pro  
                                  45

## (2) INFORMATION FOR SEQ ID NO: 468:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LCVFASVASCDA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu  
 -40 -35 -30 -25  
 Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe  
 -20 -15 -10  
 Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala  
 -5 1 5  
 Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro  
 10 15 20  
 Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu  
 25 30 35 40  
 Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr  
 45 50 55  
 Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser  
 60 65 70  
 Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn  
 75 80 85  
 Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser  
 90 95 100  
 Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr  
 105 110 115 120  
 Leu

## (2) INFORMATION FOR SEQ ID NO: 469:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -122...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq RLVVVSVSPQSRA/SL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

Met Ala Ser Pro Phe Ser Gly Ala Leu Gln Leu Thr Asp Leu Asp Asp  
 -120 -115 -110



Phe Ile Gly Pro Ser Gln Glu Cys Ile Lys Pro Val Lys Val Glu Lys  
 -105 -100 -95  
 Arg Ala Gly Ser Gly Val Ala Lys Ile Arg Ile Glu Asp Asp Gly Ser  
 -90 -85 -80 -75  
 Tyr Phe Gln Ile Asn Gln Asp Gly Xaa Thr Arg Arg Leu Glu Lys Ala  
 -70 -65 -60  
 Lys Val Ser Leu Asn Tyr Cys Xaa Ala Cys Ser Gly Cys Ile Thr Ser  
 -55 -50 -45  
 Ala Glu Thr Val Leu Ile Thr Gln Gln Ser His Glu Glu Leu Lys Lys  
 -40 -35 -30  
 Val Leu Asp Ala Asn Lys Met Ala Ala Pro Ser Gln Gln Arg Leu Val  
 -25 -20 -15  
 Val Val Ser Val Ser Pro Gln Ser Arg Ala Ser Leu Ala Ala Arg Phe  
 -10 -5 1 5  
 Gln Leu Xaa Pro Thr Asp Thr Ala Arg Lys Leu Thr Ser Phe Phe Lys  
 10 15 20

## (2) INFORMATION FOR SEQ ID NO: 470:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq SLVAELLLGAGSG/SH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

Met Gly Pro Val Pro Thr Ala Val Ala Gly Ala Gly Ser Arg Leu Val  
 -40 -35 -30  
 Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser  
 -25 -20 -15  
 Leu Val Ala Glu Leu Leu Leu Gly Ala Gly Ser Gly Ser His Leu Gly  
 -10 -5 1  
 Arg Ala Trp Ser Gly Leu Gly Ser Ser Ile Ile Glu Ala Ile Val Gly  
 5 10 15 20

Val Leu Leu Thr Ile Arg Pro Ser Arg Leu Glu Pro Pro Tyr His Trp  
                           25                          30                          35  
 Thr Ser Pro Ala  
                           40

## (2) INFORMATION FOR SEQ ID NO: 471:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq QFILLGTTSVVTA/AL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly  
                   -20                          -15                          -10  
 Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys  
                   -5                                  1                                  5  
 Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly  
   10                                  15                                  20                                  25  
 Glu Asp Leu Lys Ser Ile Leu Ser Glu Xaa Pro Gly Lys Cys Val Pro  
                           30                                  35                                  40  
 Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn  
                   45                                  50                                  55  
 Ser Gln Phe Val Glu Asn Cys Lys  
                   60                                  65

## (2) INFORMATION FOR SEQ ID NO: 472:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq IYIICFXLPPLFS/FN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Gln Val Cys Arg Cys Ile Tyr Ile Ile Cys Phe Xaa Leu Pro Pro  
                   -15                  -10                  -5

Leu Phe Ser Phe Asn  
                   1

## (2) INFORMATION FOR SEQ ID NO: 473:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq QRLLLRFLASVIS/RK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Ala Gln Arg Leu Leu Leu Arg Phe Leu Ala Ser Val Ile Ser Arg  
   -15                  -10                  -5                  1

Lys Pro Ser Gln Gly Gln Trp Ala Thr Pro His Phe Gln Ser Pro Ala  
                   5                  10                  15

Asp Pro Thr Met Gln Ser Trp Trp Pro Asp Cys Asn Thr Gln Pro Ser  
           20                  25                  30

Pro Asp  
       35

## (2) INFORMATION FOR SEQ ID NO: 474:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq FLWLITRQPVLPL/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Met Leu Phe Ile Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala  
-40 -35 -30 -25  
Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile  
-20 -15 -10  
Thr Arg Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Xaa  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -46..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq SHMLQLLPSKALC/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Tyr Pro Lys Trp Glu Ala Pro Val Thr Phe Cys Gln Leu Lys Arg  
-45 -40 -35  
Gln Lys Asp Pro Pro His Pro Ala His Ser Pro Phe Leu Gln Pro Arg  
-30 -25 -20 -15



(D) OTHER INFORMATION: score 13.8  
seq XGLLLFLLPGSLG/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Gly Val Pro Arg Pro Gln Pro Trp Ala Xaa Gly Leu Leu Leu Phe
      -20                      -15                      -10

Leu Leu Pro Gly Ser Leu Gly Ala Glu Ser His Leu Ser Leu Leu Tyr
      -5                      1                      5

His Leu Thr Ala Val Ser Ser Pro Ala Pro Gly Thr Pro Ala Phe Trp
  10                      15                      20                      25

Val Ser Gly Trp Leu Gly Pro Gln Gln Tyr Pro Ser Xaa
      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.4  
seq LVLALXLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

```

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys
-45                      -40                      -35                      -30

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
      -25                      -20                      -15

Leu Val Leu Ala Leu Xaa Leu Val Ser Ala Ala Leu Ser Ser Val Val
      -10                      -5                      1

Ser Arg Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser
  5                      10                      15

Thr Pro Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser
  20                      25                      30                      35

Ile Ser Gln Ile Ser Thr Thr Leu Pro Pro Xaa Xaa Ser Thr Lys Xaa
      40                      45                      50

```

Ser Gly Gly Ala Xaa Val Val Pro His Pro Ser Pro Gly  
                   55                                  60

## (2) INFORMATION FOR SEQ ID NO: 479:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13  
seq LLLVLLLVTXRS/MP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe  
                   -25                                  -20                                  -15

Leu Leu Leu Val Leu Leu Leu Val Thr Arg Xaa Arg Ser Met Pro Ala  
                   -10                                  -5                                  1

Ser Ser Pro Ala Ala Ser Ser Phe Tyr Cys Ala Ser Ser Ala Xaa Ser  
           5                                  10                                  15

Arg Cys Pro Leu Ala Gly Pro Cys Arg Cys Ser Ser Pro Gly Thr Ala  
   20                                  25                                  30                                  35

Phe Leu

## (2) INFORMATION FOR SEQ ID NO: 480:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.6  
seq LLLLVQLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

```

Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
   -25                      -20                      -15

Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
   -10                      -5                      1

Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
   5                      10                      15                      20

Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
   25                      30                      35

Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
   40                      45                      50

Ala Arg

```

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2  
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

```

Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser
-20                      -15                      -10                      -5

Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
   1                      5                      10

Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
   15                      20                      25

Gly Asp Gln Leu Ile Trp Thr Arg
   30                      35

```



## (2) INFORMATION FOR SEQ ID NO: 482:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2  
seq AFLLLVALSYTLA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Ser Asn Tyr Thr Asp Ala Glu Ser Ser Phe Ser Lys Gln Glu Ile  
-40 -35 -30 -25  
Ile Arg Val Ala Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu  
-20 -15 -10  
Val Ala Leu Ser Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly  
-5 1 5  
Ala Lys Lys Asp Thr Lys Asp Ser Arg Pro Lys Pro Pro Arg  
10 15 20

## (2) INFORMATION FOR SEQ ID NO: 483:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -53..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6  
seq FILLIFIAEVAA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Phe | Xaa | Thr | Trp | Ala | Thr | Ser | Ser | Gln | Pro | Ala | Leu | Trp |     |
|     |     |     | -50 |     |     |     |     | -45 |     |     |     |     | -40 |     |     |
| Ser | Leu | Leu | Leu | Val | Ser | Trp | Ala | Ala | Met | Val | Leu | Arg | Leu | Arg | Ser |
|     |     | -35 |     |     |     |     | -30 |     |     |     |     | -25 |     |     |     |
| Lys | Cys | Ala | Leu | Val | Thr | Phe | Phe | Phe | Ile | Leu | Leu | Leu | Ile | Phe | Ile |
|     | -20 |     |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |
| Ala | Glu | Val | Ala | Ala | Ala | Val | Val | Ala | Leu | Val | Tyr | Xaa | Thr | Met | Xaa |
| -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |
| Glu | His | Phe | Leu | Thr | Leu | Leu | Val | Val | Pro | Ala | Ile | Lys | Lys | Asp | Tyr |
|     |     | 15  |     |     |     |     |     | 20  |     |     |     |     | 25  |     |     |
| Gly | Ser | Gln | Glu | Asp | Phe | Thr | Gln | Val | Xaa | Asn | Thr | Thr | Met | Lys | Gly |
|     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |
| Leu | Lys | Cys | Cys | Gly | Phe | Thr | Asn | Tyr | Thr | Asp | Trp |     |     |     |     |
|     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -28..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.5  
seq LLLLVHLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Trp | Glu | Leu | Leu | Leu | Trp | Leu | Leu | Val | Leu | Cys | Ala | Leu | Leu |
|     |     |     | -25 |     |     |     |     | -20 |     |     |     |     | -15 |     |     |
| Leu | Leu | Leu | Val | His | Leu | Leu | Arg | Phe | Leu | Arg | Ala | Asp | Gly | Asp | Leu |
|     |     | -10 |     |     |     |     | -5  |     |     |     |     | 1   |     |     |     |
| Thr | Leu | Leu | Trp | Ala | Glu | Trp | Gln | Gly | Arg | Arg | Pro | Glu | Trp | Glu | Leu |
| 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     | 20  |
| Thr | Asp | Met | Val | Val | Trp | Val | Thr | Gly | Ala | Ser | Ser | Gly | Ile | Gly | Glu |
|     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |     | 35  |     |
| Glu | Leu | Ala | Tyr | Gln | Leu | Ser | Lys | Leu | Gly | Xaa | Ser | Leu | Val | Leu | Ser |
|     |     | 40  |     |     |     |     |     | 45  |     |     |     |     | 50  |     |     |

Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu  
           55                                60                                65

Asn Gly Asn Leu Xaa Glu Lys Asp Ile Leu Val Leu Pro Leu Gly  
       70                                75                                80

## (2) INFORMATION FOR SEQ ID NO: 485:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.3  
seq VSCLTLWSPGCWP/QP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Thr Thr Phe Leu Pro Val Pro Gln Met Met Ala Gly Phe Ser Phe  
       -50                                -45                                -40

Gly Thr Phe Gly Asn Pro Pro Met Glu Ser Pro Ser Ala Trp Gln Thr  
       -35                                -30                                -25                                -20

Ile His Gln Pro Phe Ile Val Ser Cys Leu Thr Leu Trp Ser Pro Gly  
                                 -15                                -10                                -5

Cys Trp Pro Gln Pro Ile Gln Arg Lys Glu Trp Asp Ser Gly Thr Phe  
                                 1                                5                                10

Glu Asn Leu Arg Val Leu Ser Cys Ala Met Val Glu  
       15                                20                                25

## (2) INFORMATION FOR SEQ ID NO: 486:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq LVXFSL LATAILG/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```

Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln Leu
   -25               -20               -15

Val Xaa Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser Trp
   -10               -5               1

Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu Pro
   5               10               15               20

Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys Leu
   25               30               35

Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys
   40               45               50

Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln Glu
   55               60               65

Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe Phe
   70               75               80

Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly
   85               90               95               100

Leu

```

## (2) INFORMATION FOR SEQ ID NO: 487:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq VLPVILL LLLGAHP/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu  
 -20 -15 -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala  
 -5 1 5 10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Xaa Pro Ile Pro Ser  
 15 20 25

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr  
 30 35 40

Ile Phe Leu Lys Phe Asp Gly Glu Arg  
 45 50

## (2) INFORMATION FOR SEQ ID NO: 488:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -109..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1  
seq LVLAVLFFHQLVG/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val Ala Leu  
 -105 -100 -95

Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro Arg Leu  
 -90 -85 -80

Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Xaa Lys Ser Tyr Val  
 -75 -70 -65

Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu Leu  
 -60 -55 -50

Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr  
 -45 -40 -35 -30

Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu  
 -25 -20 -15

Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu  
 -10 -5 1

Lys

## (2) INFORMATION FOR SEQ ID NO: 489:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq LLLLCALHSHIYC/IK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

Met Pro Asn Leu Ser Phe Gly Gly Leu Asp Thr Asn Gln Met Arg Val  
-35 -30 -25

Asn Phe Leu Ser Val Asp Val Cys Lys Leu Leu Leu Leu Cys Ala Leu  
-20 -15 -10

His Ser His Ile Tyr Cys Ile Lys Gln Ser Ala Leu Arg  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 490:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq XXLLLLNVGQLLA/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```

Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu
-55                      -50                      -45                      -40

Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu
                      -35                      -30                      -25

Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Xaa Xaa Leu Leu Leu Leu
                      -20                      -15                      -10

Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr
                      -5                      1                      5

Arg Lys Lys Thr Leu Ser Thr
10                      15

```

## (2) INFORMATION FOR SEQ ID NO: 491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -71..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6  
seq VVXFLLLLLAXLIA/TY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

```

Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg Arg
-70                      -65                      -60

Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu Ile
-55                      -50                      -45                      -40

Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu Trp
                      -35                      -30                      -25

Thr Ser Lys Leu Trp His Arg Xaa Xaa Ile Val Val Xaa Phe Leu Leu
                      -20                      -15                      -10

Leu Leu Ala Xaa Leu Ile Ala Thr Tyr Tyr
-5                      1

```

## (2) INFORMATION FOR SEQ ID NO: 492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq LLRGLLWXQVLCA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

```
Met Pro Leu Leu Arg Gly Leu Leu Trp Xaa Gln Val Leu Cys Ala Gly
-15                -10                -5                1

Pro Leu His Thr Glu
                5
```

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.4  
seq AVVGCLLVPPAEA/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

```
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
-20                -15                -10                -5

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Xaa Cys Lys Cys Ile
                1                5                10

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
                15                20                25

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
                30                35                40
```



Pro  
45

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg  
                  -20                  -15                  -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro  
                  -5                          1                          5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala  
          10                          15                          20

Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala  
          25                          30                          35                          40

Val Gly Glu Lys Arg  
                  45

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: -108...-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.9  
 seq LLGLLSAEQLAEA/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

```

Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val
-105                               -100                               -95

Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly
-90                               -85                               -80

Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile
-75                               -70                               -65

Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly
-60                               -55                               -50                               -45

Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val
-40                               -35                               -30

Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Xaa Xaa Val Gln Leu
-25                               -20                               -15

Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile
-10                               -5                               1

Leu Phe Asn Lys Ile Asp Asn
5                               10

```

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -41...-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.7  
 seq LLCLGQLHHPGLG/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

```

Met Glu Leu Pro Ala Val Asn Leu Glu Ser Asp Ser Pro Arg Ser Leu
-40                               -35                               -30

Ala Ala Asp Asn Leu Gly Leu His Cys Ile Leu Arg Leu Leu Cys Leu

```



(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -29..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.6  
 seq PTLAIALAANAWA/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

```

Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser Pro Thr Trp Asp Asp
      -25                      -20                      -15

Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala Trp Ala Phe Val Leu
      -10                      -5                      1

Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr Lys Ser Ser Pro Glu
      5                      10                      15

Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg Asp Leu
      20                      25                      30
  
```

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -32..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.6  
 seq WILVLALPLTVWP/WL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

```

Met Gln Gln Ile Phe Ile Gln Gln Cys Arg Glu Leu Asn Phe Trp Ser
      -30                      -25                      -20

Arg Glu Pro Trp Ile Leu Val Leu Ala Leu Pro Leu Thr Val Trp Pro
      -15                      -10                      -5

Trp Leu Ser Pro Glu Ala Gln Pro Pro Leu
      1                      5                      10
  
```

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 88 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.5  
seq AVLLALLMAGLAL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

```

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
-15                -10                -5                1
Pro Gly Thr Ala Leu Leu Cys Tyr Ser Trp Xaa Ala Gln Val Xaa Asn
      5                10                15
Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
      20                25                30
Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
      35                40                45
Gly Cys Ser Leu Asn Cys Val Asp Xaa Ser Gln Asp Tyr Tyr Val Gly
      50                55                60                65
Lys Lys Asn Ile Thr Cys Cys Asp
                        70

```

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.1  
seq QACLLGLFALILS/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu Ser  
 -15 -10 -5

Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu Pro  
 1 5 10 15

Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu Ser  
 20 25 30

Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu Leu  
 35 40 45

Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr Leu  
 50 55 60

Thr Arg  
 65

## (2) INFORMATION FOR SEQ ID NO: 502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
 seq LGSGGLGLSPGTSS/GR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Arg Pro Gly Gln Val Ser Leu Leu Gly Pro Asp Ala Val Ser Val  
 -25 -20 -15

Leu Gly Ser Gly Leu Gly Leu Ser Pro Gly Thr Ser Ser Gly Arg Asn  
 -10 -5 1

Pro Asp Pro Gly Ser Gly Pro Gly Thr Leu Pro Xaa Xaa Ser Xaa Gln  
 5 10 15

Asn Pro Ser Pro Ala Pro Asp Pro Pro Pro Ala Leu Leu Leu Trp Asn  
 20 25 30 35

Leu Leu Thr Gln Arg Leu Gly Thr Thr Leu Val Pro Thr Leu Cys Pro  
 40 45 50

Ala Gln Thr Leu Ile Leu Cys Pro Ala Gln Thr Leu Ile Leu Cys Pro  
 55 60 65

Xaa Leu Ile Pro Thr Leu Cys Pro Ala Leu Xaa Pro Val Leu Pro Xaa  
70 75 80  
Val Ala Leu Ser Ala Gln Pro Ser Leu Pro Ala Arg Val Gln Ser  
85 90 95

## (2) INFORMATION FOR SEQ ID NO: 503:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8  
seq FTSASLLLPSTG/MP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Ile Asn Pro Ser Val Pro Ser Lys Ser Asn Ser His Pro Phe Leu  
-30 -25 -20  
Ser Thr Val Met Phe Thr Ser Ala Ser Leu Leu Leu Pro Met Ser Thr  
-15 -10 -5  
Gly Met Pro Thr Gln Asn Cys Phe Thr Pro Lys  
1 5 10

-

## (2) INFORMATION FOR SEQ ID NO: 504:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -68..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7

seq IACLAWWIGGGSG/XN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Met Ser Glu Lys Glu Xaa Asn Phe Pro Pro Leu Pro Lys Phe Ile Pro  
                   -65                  -60                  -55

Val Lys Pro Cys Phe Tyr Gln Asn Phe Ser Asp Glu Ile Pro Val Glu  
                   -50                  -45                  -40

His Gln Val Leu Val Lys Arg Ile Tyr Arg Leu Trp Met Phe Tyr Cys  
                   -35                  -30                  -25

Ala Thr Leu Gly Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile Gly  
                   -20                  -15                  -10                  -5

Gly Gly Ser Gly Xaa Asn Phe Gly Leu Ala Phe Val Trp Leu Leu Leu  
                           1                  5                  10

Phe Thr Pro Cys Gly Tyr Val Cys Trp Phe Arg Pro Val Tyr Lys Ala  
                   15                  20                  25

Phe Arg Ala Asp Ser Ser Phe Asn Phe Met Ala Leu  
                   30                  35                  40

## (2) INFORMATION FOR SEQ ID NO: 505:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
                                   seq ILRLYFFFLQLAHS/GY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

Met Asn Pro Thr Lys Leu Ile Leu Lys Thr Ile Leu Arg Leu Tyr Phe  
                   -20                  -15                  -10

Phe Leu Gln Leu Ala His Ser Gly Tyr Thr Lys Leu Gln Lys Lys Tyr  
                   -5                  1                  5

Met Lys Ser Arg Tyr Glu Gln Val Asp Leu Val Gly Lys Met Xaa Gln  
                   10                  15                  20                  25

Lys Ala Ala Thr Thr Val Xaa His Leu Ala Ile Gln Cys His Trp